

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 17:17:11 ; Search time 685.5 Seconds
(without alignments)
1770.394 Million cell updates/sec

Title: US-10-085-944-1

Perfect score: 28
Sequence: 1 cccatctcannatccctgtgttg 28

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_hgt:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sta:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vt:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pi:*
- 26: em_ro:*
- 27: em_sta:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_man:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_higo_hum:*
- 40: em_higo_mus:*
- 41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	25	89.3	2319	14	S66064	S66064 structural
C 2	25	89.3	2325	14	AF469175	AF469175 Dengue v1
C 3	25	89.3	2325	14	AF469176	AF469176 Dengue v1
C 4	25	89.3	2357	6	AR232496	AR232496 Sequence
C 5	25	89.3	2357	14	DEN2NGC	DEN2NGC Dengue viru
C 6	25	89.3	2552	14	AY152036S1	AY152036 Dengue v1
C 7	25	89.3	2552	14	AY152040S1	AY152040 Dengue v1
C 8	25	89.3	2552	14	AY152044S1	AY152044 Dengue v1
C 9	25	89.3	2552	14	AY152048S1	AY152048 Dengue v1
C 10	25	89.3	2552	14	AY152052S1	AY152052 Dengue v1
C 11	25	89.3	2552	14	AY152056S1	AY152056 Dengue v1
C 12	25	89.3	2552	14	AY152060S1	AY152060 Dengue v1
C 13	25	89.3	2552	14	AY152064S1	AY152064 Dengue v1
C 14	25	89.3	2552	14	AY152068S1	AY152068 Dengue v1
C 15	25	89.3	2552	14	AY152072S1	AY152072 Dengue v1
C 16	25	89.3	2552	14	AY152076S1	AY152076 Dengue v1
C 17	25	89.3	2552	14	AY152080S1	AY152080 Dengue v1
C 18	25	89.3	2552	14	AY152084S1	AY152084 Dengue v1
C 19	25	89.3	2552	14	AY152088S1	AY152088 Dengue v1
C 20	25	89.3	2552	14	AY152092S1	AY152092 Dengue v1
C 21	25	89.3	2552	14	AY152100S1	AY152100 Dengue v1
C 22	25	89.3	2552	14	AY152104S1	AY152104 Dengue v1
C 23	25	89.3	2552	14	AY152108S1	AY152108 Dengue v1
C 24	25	89.3	2552	14	AY152112S1	AY152112 Dengue v1
C 25	25	89.3	2552	14	AY152116S1	AY152116 Dengue v1
C 26	25	89.3	2552	14	AY152120S1	AY152120 Dengue v1
C 27	25	89.3	2552	14	AY152124S1	AY152124 Dengue v1
C 28	25	89.3	2552	14	AY152128S1	AY152128 Dengue v1
C 29	25	89.3	2552	14	AY152132S1	AY152132 Dengue v1
C 30	25	89.3	2552	14	AY152136S1	AY152136 Dengue v1
C 31	25	89.3	2552	14	AY152144S1	AY152144 Dengue v1
C 32	25	89.3	2552	14	AY152148S1	AY152148 Dengue v1
C 33	25	89.3	2552	14	AY152152S1	AY152152 Dengue v1
C 34	25	89.3	2552	14	AY152156S1	AY152156 Dengue v1
C 35	25	89.3	2552	14	AY152160S1	AY152160 Dengue v1
C 36	25	89.3	2552	14	AY152164S1	AY152164 Dengue v1
C 37	25	89.3	2552	14	AY152168S1	AY152168 Dengue v1
C 38	25	89.3	2552	14	AY152172S1	AY152172 Dengue v1
C 39	25	89.3	2552	14	AY152176S1	AY152176 Dengue v1
C 40	25	89.3	2552	14	AY152180S1	AY152180 Dengue v1
C 41	25	89.3	2552	14	AY152184S1	AY152184 Dengue v1
C 42	25	89.3	2552	14	AY152188S1	AY152188 Dengue v1
C 43	25	89.3	2552	14	AY152192S1	AY152192 Dengue v1
C 44	25	89.3	2552	14	AY152196S1	AY152196 Dengue v1
C 45	25	89.3	2552	14	AY152200S1	AY152200 Dengue v1

ALIGNMENTS

RESULT 1
S66064/c
LOCUS
DEFINITION
S66064 structural polypeptide (dengue type 4 virus DEN4, H241-P, Genomic,
2319 nt).
ACCESSION
S66064
VERSION
S66064.1 GI:432575
KEYWORDS
SOURCE
Dengue virus type 4
ORGANISM
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2319)
AUTHORS
Kawano,H., Rostapshov,V., Rosen,L. and Lai,C.J.
TITLE
Genetic determinants of dengue type 4 virus neurovirulence for mice

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J. Virol. 67 (11), 6567-6575 (1993)
MEDLINE 94016840
PUBMED 8411360
REMARK GenBank staff at the National Library of Medicine created this
        entry [NCBI gisseq 138430] from the original journal article.
        This sequence comes from Fig. 1.
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Best Local Similarity 89.3%; Pred. No. 0.89;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCNTCANNATCCCTGCTGTTGG 28
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DB 205 CCCATCTCTTCAGAAATCCCTGCTGTTGG 178

RESULT 2
AF469175/c
LOCUS      Dengue virus type 2 strain GD24/93 polypeptide gene, partial cds.
DEFINITION
ACCESSION  AF469175
VERSION     AF469175.1 GI:18766554
KEYWORDS
SOURCE
ORGANISM   Dengue virus type 2
            Dengue virus type 2
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Dengue virus group.
REFERENCE  1 (bases 1 to 2325)
AUTHORS    Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
            Zhao,W.Z.
TITLE      Structural genes of dengue virus type 2 strain GD24/93 isolate from
            Nanhai, Guangdong, China
JOURNAL
REFERENCE  2 (bases 1 to 2325)
AUTHORS    Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
            Zhao,W.Z.
TITLE      Direct Submission
JOURNAL    Submitted (16-JAN-2002) Department of Virology, The Military
            Medical Institute of Guangzhou Military District, Dong Guanzhuang
            Road 91, Guangzhou, Guangdong 5105407, China
FEATURES             source
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SNWIOKETLWTFKNPHAKQDVVVGSGOEGAMHTALTGATEIQMSSGNLLFTFHLKCR
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ORIGIN
Query Match      89.3%; Score 25; DB 14; Length 2325;
Best Local Similarity 89.3%; Pred. No. 0.89;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCNTCANNATCCCTGCTGTTGG 28
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DB 208 CCCATCTCTTCATATCCCTGCTGTTGG 181

RESULT 3
AF469176/c
LOCUS      Dengue virus type 2 strain GD08/98 polypeptide gene, partial cds.
DEFINITION
ACCESSION  AF469176
VERSION     AF469176.1 GI:18766556
KEYWORDS
SOURCE
ORGANISM   Dengue virus type 2
            Dengue virus type 2
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Dengue virus group.
REFERENCE  1 (bases 1 to 2325)
AUTHORS    Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
            Zhao,W.Z.
TITLE      Structural genes of dengue virus type 2 strain GD24/93 isolate from
            Nanhai, Guangdong, China
JOURNAL
REFERENCE  2 (bases 1 to 2325)
AUTHORS    Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
            Zhao,W.Z.
TITLE      Direct Submission
JOURNAL    Submitted (16-JAN-2002) Department of Virology, The Military
            Medical Institute of Guangzhou Military District, Dong Guanzhuang
            Road 91, Guangzhou, Guangdong 5105407, China
FEATURES             source
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                     /mol_type="genomic RNA"
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                     /db_xref="taxon:11060"
     country="China: Nanhai, Guangdong province"
     notes="isolated from dengue haemorrhagic fever patient"
     <1..>2325
     /notes="contains structural C, M and E proteins"
     /codon_start=1
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ORIGIN

Query Match 89.3%; Score 25; DB 14; Length 2325;
Best Local Similarity 89.3%; Pred. No. 0.89;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
DB 208 CCCATCTCTCAATATCCCTGCTGTGG 181

RESULT 4

AR232496/c AR232496 2357 bp RNA linear PAT 20-DEC-2002
LOCUS Sequence 1 from patent US 6455509.
DEFINITION AR232496
ACCESSION AR232496
VERSION AR232496.1 GI:27274633
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE

1 (bases 1 to 2357)
Kocheil,T.J., Porter,K.R., Raviprakash,K., Hoffman,S.L. and
Hayes,C.G.
Dengue nucleic acid vaccines that induce neutralizing antibodies
Patent: US 6455509-A 1 24-SEP-2002;
Location/Qualifiers
1. .2357
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/mol_type="genomic RNA"

ORIGIN

Query Match 89.3%; Score 25; DB 6; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.89;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
DB 228 CCCATCTCTCAGTATCCCTGCTGTGG 201

RESULT 5

DEN2NGC/c DEN2NGC 2357 bp RNA linear VRL 29-MAY-2002
LOCUS Dengue virus type 2 gene for polyprotein, partial cds, strain:New
DEFINITION Guinea C.
ACCESSION D00346
VERSION D00346.1 GI:221230
KEYWORDS
SOURCE
ORGANISM Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE

1 (bases 1 to 2357)
Gruenberg,A., Woo,W.S., Biedrzycka,A. and Wright,P.J.
Partial nucleotide sequence and deduced amino acid sequence of the
structural proteins of dengue virus type 2, New Guinea C and
PUO-218 strains
J. Gen. Virol. 69 (Pt 6), 1391-1398 (1988)
JOURNAL 88258474
MEDLINE

3385407

PUBMED
COMMENT Nucleotide 1 in the NGC sequence corresponds to nucleotide 77
counting from the 5' end of the DEN-2(JAM) sequence.

FEATURES

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LRMDKLQKMGSMYSCMTGKFKVKEIAETQHGTVIRVQYEGDGPCKIPFIMDLER
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CDS

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ORIGIN

Query Match 89.3%; Score 25; DB 14; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.89;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
DB 228 CCCATCTCTCAGTATCCCTGCTGTGG 201

RESULT 6

AY152036S1/c AY152036S1 2552 bp RNA linear VRL 29-SEP-2003
LOCUS Dengue virus type 4 D4.20_1998 polyprotein precursor, gene, partial
DEFINITION cds.
ACCESSION AY152036
VERSION AY152036.1 GI:28170806
KEYWORDS
SEGMENT 1 of 4
SOURCE Dengue virus type 4 (DEN-4)
ORGANISM Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE

1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vornadam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,

Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico

FEATURES
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ORIGIN
Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTTTGG 28
Db 205 CCCATCTCTCAGAAATCCCTGCTTTGG 178

RESULT 7
AY152040S1/C
LOCUS AY152040S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.19_1998 polyprotein precursor, gene, partial
cda.
ACCESSION AY152040
VERSION AY152040.1 GI:28170815
KEYWORDS
SEGMENT 1 of 4
SOURCE
ORGANISM
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
source
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LRTYCIASISNITTATRCPTQGPYLVKEEQDQYICRRDVDRMGWGCGLFGKGV
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KVGVRVISTPLAENTSVNIELEPPFGDSYIVIGNSALTLHFRKSGSIGKMPF
STYRGAKMAILIAGETAWDFSGVGLFTSLGKAVHQVFGSVYTTMFGVGSWMIRILIGF
LVLWIGTNSRNTSMAMTCIAGVGITLFLGFTVQADMGCVVSWSGRELKCGSGIFVGDN
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ORIGIN
Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTTTGG 28
Db 205 CCCATCTCTCAGAAATCCCTGCTTTGG 178

RESULT 8
AY152044S1/C
LOCUS AY152044S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.18_1998 polyprotein precursor, gene, partial
cda.
ACCESSION AY152044
VERSION AY152044.1 GI:28170824
KEYWORDS
SEGMENT 1 of 4
SOURCE
ORGANISM
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
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REFERENCE 2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
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1. .2552
/note="contains core protein, matrix protein and envelope
glycoprotein"

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DB	205	CCCATCTCTTCAGAAATCCCTGCTGTTGG	178			
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DEFINITION	AY152052S1	Dengue virus type 4 D4.12_1998	polyprotein precursor, gene, partial cds.	2552 bp	RNA	linear
ACCESSION	AY152052					
VERSION	AY152052.1	GI:28170842				
KEYWORDS						
SEGMENT						
SOURCE	1 of 4					
ORGANISM	Dengue virus type 4 (DEN-4)					
REFERENCE	Viruses; SARNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.					
AUTHORS	1 (bases 1 to 2552)					
TITLE	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.					
JOURNAL	Selection-Driven Evolution of Emergent Dengue Virus					
PUBMED	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)					
REFERENCE	12832629					
AUTHORS	2 (bases 1 to 2552)					
TITLE	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.					
JOURNAL	Direct Submission					
FEATURES	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico					
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ORIGIN

Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCNTCANNATCCCTGCTGTGG 28
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DB 205 CCCATCTCTTCAGAAATCCCTGCTGTGG 178

RESULT 11

AY152056S1/c
LOCUS AY152056S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.17_1998 polyprotein precursor, gene, partial cds.

ACCESSION AY152056

VERSION AY152056.1 GI:28170851

KEYWORDS 1 of 4

SOURCE Dengue virus type 4 (DEN-4)

ORGANISM

Dengue virus type 4
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE 1 (bases 1 to 2552)

AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,

Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.

TITLE Selection-Driven Evolution of Emergent Dengue Virus

JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

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REFERENCE 2 (bases 1 to 2552)

AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,

Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.

TITLE Direct Submission

JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio

Piedras, PO Box 23360, San Juan 00931, Puerto Rico

FEATURES

source

1. .2552

Location/Qualifiers

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ORIGIN

Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCNTCANNATCCCTGCTGTGG 28
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DB 205 CCCATCTCTTCAGAAATCCCTGCTGTGG 178

RESULT 12

AY152060S1/c
LOCUS AY152060S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.45_1998 polyprotein precursor, gene, partial cds.

ACCESSION AY152060

VERSION AY152060.1 GI:28170860

KEYWORDS 1 of 4

SEGMENT Dengue virus type 4 (DEN-4)

SOURCE Dengue virus type 4

ORGANISM

Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE 1 (bases 1 to 2552)

AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,

Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.

TITLE Selection-Driven Evolution of Emergent Dengue Virus

JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

PUBMED 12832629

REFERENCE 2 (bases 1 to 2552)

AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,

Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.

TITLE Direct Submission

JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio

Piedras, PO Box 23360, San Juan 00931, Puerto Rico

FEATURES

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Location/Qualifiers

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ORIGIN

Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 205 CCCATCTCTTCAGATCCCTGCTGTGG 178

RESULT 13
LOCUS AY152064S1/c 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.47_1998 polyprotein precursor, gene, partial cds.
ACCESSION AY152064
VERSION AY152064.1 GI:28170869
KEYWORDS
SEGMENT
SOURCE
ORGANISM

1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
REFERENCE
2 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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ORIGIN
Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
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Db 205 CCCATCTCTTCAGATCCCTGCTGTGG 178

RESULT 14
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DEFINITION Dengue virus type 4 D4.13_1998 polyprotein precursor, gene, partial cds.
ACCESSION AY152072
VERSION AY152072.1 GI:28170887
KEYWORDS
SEGMENT
SOURCE
ORGANISM

1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
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Location/Qualifiers
REFERENCE
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Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
FEATURES
Source
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/isolate="D4.47_1998"
/db_xref="taxon:11070"
/country="Puerto Rico"
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1..2552
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glycoprotein"
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VTCAPFSCSGKITGNLVQIENLEYTVVTVHNGDTHAVGNDTSNHGVTATITPRSPV
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VHTWTEQYKFQEPESPARLASAILNAHKDGVCGIRSTTRLENVWMKQITNELN"

ORIGIN
Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
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Db 205 CCCATCTCTTCAGATCCCTGCTGTGG 178

RESULT 15
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DEFINITION Dengue virus type 4 D4.46_1998 polyprotein precursor, gene, partial cds.
ACCESSION AY152072
VERSION AY152072.1 GI:28170887
KEYWORDS
SEGMENT
SOURCE
ORGANISM

1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
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Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
REFERENCE
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Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
FEATURES
Source
1..2552
/organism="Dengue virus type 4"
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/isolate="D4.47_1998"
/db_xref="taxon:11070"
/country="Puerto Rico"
/notes="acronym: DEN-4"
1..2552
/notes="contains core protein, matrix protein and envelope
glycoprotein"
/codon_start=1
/product="polyprotein precursor"
/protein_id="AAN38351.1"
/db_xref="GI:28170885"
/translation="MNQRKKVVRPPNMLKRRNRVSTPQGLVKRPFSTGLFSGKGLPLR
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RAETWMSSEGAKHQRVESWILRNPGFALLAGFMAYMIGOTGIORTVFPVLMVLAP
SYGMCRCVGNRDRFVEGVS GGAWDLVLEHGCVTTMAQCKTFLDFELIKTTAKEVAL
LRTYICIASISNITTATRCPTQGEPLYKEEQDQYICRDVVDRGNGCGGLFGKGGV
VTCAPFSCSGKITGNLVQIENLEYTVVTVHNGDTHAVGNDTSNHGVTATITPRSPV
EYKLPDYBELTDCPRSGIDFNEMILMKMKKTLWLHKQWFLDLPWPMTAGADTSEV
HNNYKERVMTFKVPHAKRQDVTVLGSOEGAMHSAAGATEVDSGDGNHMFAGHLKCKV
RMEKRLIKGMSVTMCSGKFSIDKMAETOHGTTVVKVYEGAGAPCKVPIEIRDVNKE
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STYRKARWAILGESTAMDFSGVGLFTSLGKAHVQVGSVYITFMFGVSWMIRILIGF
LVLTGTSNRNTSMATCIAGGITFLGFTVQADMGCVCVSWSGRELKCGSIFVVDN
VHTWTEQYKFQEPESPARLASAILNAHKDGVCGIRSTTRLENVWMKQITNELN"

ORIGIN
Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 205 CCCATCTCTTCAGATCCCTGCTGTGG 178
```

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE
AUTHORS

1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629

REFERENCE
AUTHORS

2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico

FEATURES
source

1. .2552
/organism="Dengue virus type 4"
/mol_type="genomic RNA"
/isolate="D4.46.1998"
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glycoprotein"
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TVYKPLLVNTEPEDIDCKNLSTWVMYGTCTQSGERERKRSVALTSHSGMLET
RAETWSSEGAWKHAQVESWILRNPGFALLAGFMAYMGIGIQRTVFFVLMVLVAP
SYGMRCVGNRDFVEGSGGAWVDLVLEHGGCVTTMAQKPTLDLFTKTTAKEVAL
LRTYCEASISNITTATRCPTQGEPLKEEQDQYICRRDVDRMGNGCGLFGKGV
VTCAKFSCSGKITGNLYQIENLEYTVVTVHNGDTHAVGNDTSGHGVATITPRSPV
EVKLDPYGLTLDCEPRSGIDFENMILMKKKTWLVHKKWFLDPLPWTAGADTSEV
HNNYKERMTFKVPHAKRQDVTVLGSGEGAMHSLAGATEVSDGNGHMFAGHLCKV
RMEKLRIKGSYTHCSGKFSIDKEMASTQHTTVVKVYEGAGAPCKVPIEIRDVNKE
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STYRGAKRMALGETAMDVGSLGFTSLGKAVHVFQSVYTTMFGVSWMIRILIGF
LVLWIGTNSRNTSNAMTCAVGGITLFLGFTVQADMGCVCVWSGRELKCGSGIFVVDN
VHTWTEQYKQPESPARLASAILNAHKDGVCGIRSTTRLENVNMVKQITNELN"

CDS

ORIGIN

Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.88;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCNTCANNATCCCTGCTTGG 28
Db 205 CCCATCTCTCAGAAATCCCTGCTTGG 178

Search completed: August 3, 2004, 19:08:56
Job time : 686.5 secs

Result No.	Query	Score	Match	Length	DB	ID	Description
1		25	89.3	28	7	ABX15697	Abx15697 Dengue vi
C 2		25	89.3	2357	7	ABX13740	Abx13740 Dengue vi
C 3		25	89.3	10616	7	AAD53912	Aad53912 Dengue vi
C 4		25	89.3	10649	7	AAD53911	Aad53911 Recombina
C 5		25	89.3	10649	7	AAD53910	Aad53910 Dengue vi
C 6		25	89.3	10717	4	AAD14605	Aad14605 Dengue vi
C 7		25	89.3	10723	2	AAT49303	Aat49303 cDNA sequ
C 8		25	89.3	10723	2	AAT49304	Aat49304 cDNA enco
C 9		25	89.3	10723	4	AAD14614	Aad14614 Dengue vi
C 10		25	89.3	10723	4	AAD14607	Aad14607 Wild-type
C 11		25	89.3	10723	4	AAD14606	Aad14606 Dengue vi
C 12		25	89.3	10723	4	AAD14608	Aad14608 Attenuate
C 13		25	89.3	10756	4	AAD14609	Aad14609 Dengue vi
C 14		23.4	83.6	32	2	AAT75919	Aat75919 DEN-2 clo
C 15		23.4	83.6	10648	4	AAD14612	Aad14612 Wild-type
C 16		23.4	83.6	10648	4	AAD14613	Aad14613 Attenuate
C 17		23.4	83.6	10723	2	AAQ12787	AAq12787 Dengue 2
C 18		21.8	77.9	3381	2	AAT47666	Aat47666 Dengue vi
C 19		21.8	77.9	3381	2	AAX25114	Aax25114 Dengue vi
C 20		20.2	72.1	2394	2	AAT49305	Aat49305 Nucleotid
C 21		20.2	72.1	10718	2	AAQ51476	AAq51476 DENI-S275
C 22		20.2	72.1	10723	4	AAD14603	Aad14603 Dengue vi
C 23		20.2	72.1	10723	4	AAD14604	Aad14604 Dengue vi

XX Claim 25; Page 1; 6pp; English.

XX This invention relates to novel Dengue virus reverse transcriptase (RT)

XX PCR primers which may be used to detect Dengue virus in a sample. Dengue

XX virus is a member of the flavivirus family and causes diseases including

XX dengue fever (DF) and dengue haemorrhagic fever. The invention also

XX comprises a method for detecting and quantitating dengue virus. The

XX dengue virus-specific primers of the invention are useful in reverse

XX transcriptase-polymerase chain reaction assays, particularly for

XX detecting or quantitating dengue virus in a sample. The present sequence

XX represents a dengue virus specific RT-PCR primer used in the method of

XX the invention

XX Sequence 28 BP; 3 A; 10 C; 4 G; 8 T; 0 U; 3 Other;

Query Match 89.3%; Score 25; DB 7; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.14;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTTGG 28

DB 1 CCCATCTCTCANNATCCCTGCTGTTGG 28

RESULT 2

ID ABX13740/c

AC ABX13740 standard; DNA; 2357 BP.

XX ABX13740;

XX 28-FEB-2003 (first entry)

XX Dengue virus type 2 structural gene genome segment.

XX Pharmaceutical; ds; immune response; immunogenic; envelope; membrane;

XX PreM; dengue virus; Den; serotype; flavivirus; Flaviviridae; antigen;

XX mosquito; Aedes aegyptii; acute undifferentiated fever;

XX dengue haemorrhagic fever; DHP; dengue shock syndrome; DSS;

XX immune enhancement phenomenon; DNA vaccine; gene therapy; vaccine;

XX structural gene; virucide.

XX Dengue virus.

XX US6455509-B1.

XX 24-SEP-2002.

XX 04-JUN-1997; 97US-00869423.

XX 04-JUN-1996; 96US-0017839P.

XX (USNA) US SEC OF NAVY.

XX Kochel TJ, Porter KR, Raviprakash K, Hoffman SL, Hayes CG;

XX WPI; 2003-066244/06.

XX New pharmaceutical compositions containing dengue nucleic acids, useful

XX as a vaccine, particularly for inducing a protective immune response in

XX mammalian subjects against the dengue virus infection.

XX Disclosure; Col 17-20; 26pp; English.

XX The invention discloses a pharmaceutical composition capable of inducing

XX an immune response in a mammalian subject, comprising an immunogenic

XX amount of a eukaryotic plasmid expression vector in pharmaceutical form,

XX which includes the envelope and membrane (PreM) genes of a dengue type 1,

XX 2, 3, or 4 virus. Dengue virus (Den) belongs to the flavivirus genus of

XX the family Flaviviridae and is a positive strand RNA virus encoding ten

XX proteins. These genes are translated as a polypeptide which is cleaved by

XX host and viral proteinases. The virus envelope protein is a major antigen

XX which can be targeted by neutralising antibodies. The membrane protein

CC also appears on the virion surface and is required for proper processing

CC of the envelope protein. Dengue viruses are transmitted primarily by the

CC mosquito, Aedes aegyptii, and can lead to human illnesses ranging from

CC acute undifferentiated fever to dengue haemorrhagic fever (DHF) and

CC dengue shock syndrome (DSS). Secondary infections, with a different

CC serotype, may lead to an immune enhancement phenomenon. The compositions

CC of the invention are DNA vaccines which are injected into the animal as a

CC technique of gene therapy. The composition is useful as a vaccine,

CC particularly for inducing a protective immune response in mammalian

CC subjects against the dengue virus infection. The sequence presented is

CC the dengue virus type 2 (Den 2) structural gene genome segment

XX

XX Sequence 2357 BP; 782 A; 471 C; 595 G; 509 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 7; Length 2357;

Best Local Similarity 89.3%; Pred. No. 0.29;

Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTTGG 28

DB 228 CCCATCTCTCAGTATCCCTGCTGTTGG 201

RESULT 3

AAAD53912/c

ID AAD53912 standard; DNA; 10616 BP.

XX AAD53912;

XX 28-MAY-2003 (first entry)

XX Dengue virus type 2 strain rDEN2/4delta30 DNA.

XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.

XX Dengue virus.

XX OS

XX Key 97.10263 Location/Qualifiers

XX CDS /tag= a /product= "DEN4 strain rDEN2/4delta30 protein"

FT mat_peptide /tag= c /product= "Anchored capsid protein"

FT mat_peptide /tag= b /product= "Virion capsid protein"

FT mat_peptide /tag= d /product= "Membrane precursor protein"

FT mat_peptide /tag= e /product= "Membrane protein"

FT mat_peptide /tag= f /product= "Envelope protein"

FT mat_peptide /tag= g /product= "NS1 protein"

FT mat_peptide /tag= h /product= "NS2A protein"

FT mat_peptide /tag= i /product= "NS2B protein"

FT mat_peptide /tag= j /product= "NS3 protein"

FT mat_peptide /tag= k /product= "NS4A protein"

FT mat_peptide /tag= l

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FT mat_peptide /product= "2K protein"
FT 6826..7560
FT /*tag= m
FT
FT mat_peptide /product= "NS4B protein"
FT 7561..10260
FT /*tag= n
FT /product= "NS5 protein"
FT
XX
PN WO200295075-A1.
XX
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-US016308.
XX
XX 22-MAY-2001; 2001US-0293049P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (BLAN/) BLANEY J E.
XX
XX Whitehead SS, Murphy BR, Hanley KA;
XX
XX WPI; 2003-120809/11.
XX P-PSDB; AAE35314.
XX
XX New mutated flavivirus, useful for fine tuning the attenuation and growth
XX characteristics of dengue virus vaccines for the prevention and/or
XX treatment of dengue virus infection.
XX
XX Disclosure; Page 135-138; 246pp; English.
XX
XX The present invention relates to novel mutated flaviviruses comprising a
XX phenotype in which the viral genome is modified by introduction of a
XX mutation, singly or in combination, taken from mutations from recombinant
XX virus bearing Vero adaptation mutations, putative Vero cell adaptation
XX mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
XX dengue type 4 virus. The methods and compositions of the invention are
XX useful for fine tuning the attenuation and growth characteristics of
XX dengue virus vaccines for the prevention and/or treatment of dengue virus
XX infection. The present sequence is Dengue virus type 4 strain
XX rDEN2/4delta30 DNA
XX
XX Sequence 10616 BP; 3365 A; 2219 C; 2743 G; 2289 T; 0 U; 0 Other;
XX
XX Query Match 89.3%; Score 25; DB 7; Length 10616;
XX Best Local Similarity 89.3%; Pred. No. 0.37;
XX Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 CCCATCTTCANNATCCCTGCTGTGG 28
DB 304 CCCATCTTCAGTATCCCTGCTGTGG 277
XX
RESULT 4
AAD53911/C
ID AAD53911 standard; DNA; 10649 BP.
XX
XX AAD53911;
XX
XX 28-MAY-2003 (first entry)
XX
XX Recombinant dengue virus type 4 strain rDEN4 DNA.
XX
XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX
XX Dengue virus.
XX
XX Key Location/Qualifiers
XX CDS 102..10649
XX /*tag= a
XX /product= "DEN4 strain rDEN4 protein"
XX 102..440
XX mat_peptide /tag= c
XX /product= "Anchored capsid protein"
XX
XX
```

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FT mat_peptide 102..398
FT /*tag= b
FT /product= "Virion capsid protein"
FT 441..938
FT /*tag= d
FT /product= "Membrane precursor protein"
FT 714..938
FT /*tag= e
FT /product= "Membrane protein"
FT 939..2423
FT /*tag= f
FT /product= "Envelope protein"
FT 2424..3479
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FT 3480..4133
FT /*tag= h
FT /product= "NS2A protein"
FT 4134..4523
FT /*tag= i
FT /product= "NS2B protein"
FT 4524..6377
FT /*tag= j
FT /product= "NS3 protein"
FT 6378..6758
FT /*tag= k
FT /product= "NS4A protein"
FT 6638..7562
FT /*tag= m
FT /product= "NS4B protein"
FT 6759..6827
FT /*tag= l
FT /product= "2K protein"
FT 7563..10262
FT /*tag= n
FT /product= "NS5 protein"
XX
XX WO200295075-A1.
XX
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-US016308.
XX
XX 22-MAY-2001; 2001US-0293049P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (BLAN/) BLANEY J E.
XX
XX Whitehead SS, Murphy BR, Hanley KA;
XX
XX WPI; 2003-120809/11.
XX P-PSDB; AAE35313.
XX
XX New mutated flavivirus, useful for fine tuning the attenuation and growth
XX characteristics of dengue virus vaccines for the prevention and/or
XX treatment of dengue virus infection.
XX
XX Disclosure; Page 131-132; 246pp; English.
XX
XX The present invention relates to novel mutated flaviviruses comprising a
XX phenotype in which the viral genome is modified by introduction of a
XX mutation, singly or in combination, taken from mutations from recombinant
XX virus bearing Vero adaptation mutations, putative Vero cell adaptation
XX mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
XX dengue type 4 virus. The methods and compositions of the invention are
XX useful for fine tuning the attenuation and growth characteristics of
XX dengue virus vaccines for the prevention and/or treatment of dengue virus
XX infection. The present sequence is Dengue virus type 4 strain rDEN4 DNA
XX
XX Sequence 10649 BP; 3298 A; 2214 C; 2804 G; 2333 T; 0 U; 0 Other;
XX
XX Query Match 89.3%; Score 25; DB 7; Length 10649;
XX Best Local Similarity 89.3%; Pred. No. 0.37;
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```
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 306 CCCATCTCTTCAGAAATCCCTGCTGTGG 279

RESULT 5
AAD53910/c
ID AAD53910 standard; DNA; 10649 BP.
XX AAD53910;
XX
XX 28-MAY-2003 (first entry)
XX Dengue virus type 4 strain 2A DNA.
XX
XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX Dengue virus.
XX
XX Key Location/Qualifiers
XX CDS 102..10649
XX /*tag= a
XX /product= "DEN4 strain 2A protein"
XX mat_peptide 102..440
XX /*tag= c
XX /product= "Anchored capsid protein"
XX mat_peptide 102..398
XX /*tag= b
XX /product= "Virion capsid protein"
XX mat_peptide 441..938
XX /*tag= d
XX /product= "Membrane precursor protein"
XX mat_peptide 714..938
XX /*tag= e
XX /product= "Membrane protein"
XX mat_peptide 939..2423
XX /*tag= f
XX /product= "Envelope protein"
XX mat_peptide 2424..3479
XX /*tag= g
XX /product= "NS1 protein"
XX mat_peptide 3480..4133
XX /*tag= h
XX /product= "NS2A protein"
XX mat_peptide 4134..4523
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XX mat_peptide 4524..6377
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XX mat_peptide 6378..6758
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XX mat_peptide 7563..10262
XX /*tag= n
XX /product= "NS5 protein"
XX
XX WO200295075-A1.
XX
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-US016308.
XX
XX 22-MAY-2001; 2001US-0293049P.
XX

Query Match 89.3%; Score 25; DB 7; Length 10649;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 306 CCCATCTCTTCAGAAATCCCTGCTGTGG 279

RESULT 6
AAD14605/c
ID AAD14605 standard; cDNA; 10717 BP.
XX AAD14605;
XX
XX 11-SEP-2003 (revised)
XX 01-NOV-2001 (first entry)
XX Dengue virus (DEN)-2/3-VP1 chimeric cDNA.
XX
XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
XX immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
XX Dengue virus; type II.
XX Dengue virus; type III.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 97..10266
XX /*tag= a
XX /product= "DEN-2/3-VP1 fusion protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
XX P-FSDB; AAE07984.
XX
```

PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.
 XX
 XX Example 2; Page 203-219; 470pp; English.
 XX
 CC The invention relates to avirulent, immunogenic flavivirus chimeras
 CC comprising amino acid mutations in the non-structural proteins of a
 CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
 CC structural genes of the virus are used as a backbone into which the
 CC structural protein genes of a second flavivirus strain are inserted.
 CC These chimeric viruses elicit pronounced immunogenicity but lack the
 CC accompanying clinical symptoms of viral disease. Attenuated chimeric
 CC flaviviruses are combined in a pharmaceutical composition to confer
 CC simultaneous immunity against several strains of pathogenic flaviviruses
 CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 CC flavivirus chimeras are also used as immunogens or multivalent vaccines
 CC to confer simultaneous protection against infections. The present cDNA
 CC sequence encodes dengue virus (DEN)-2/3-vp1 fusion protein related to the
 CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
 CC comprising a valine at the non-structural protein (NS3)-250 and the
 CC pre-membrane/membrane protein (prM) and an envelope protein (E) from wild-
 CC type DEN-3 16562 virus. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 10717 BP; 3501 A; 2208 C; 2737 G; 2271 T; 0 U; 0 Other;
 Query Match 89.3%; Score 25; DB 4; Length 10717;
 Best Local Similarity 89.3%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
 DB 304 CCCATCTCTCAATATCCCTGCTGTGG 277
 RESULT 7
 AAT49303/C
 ID AAT49303 standard; cDNA; 10723 BP.
 XX
 AC AAT49303;
 XX
 DT 27-AUG-2003 (revised)
 DT 11-SEP-1997 (first entry)
 XX
 DE cDNA sequence encoding polyprotein of DEN-2 virus, strain 16681.
 XX
 KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
 KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
 KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
 KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
 DHF; DSS; ss.
 XX
 OS Dengue virus type 2 (strain 16681).
 XX
 FH Key Location/Qualifiers
 FT CDS 97..10272
 FT /*tag= a
 FT /product= "DEN-2 polyprotein
 FT /transl_except(pos:9208..9210, aa:Xaa)"
 FT /note= "Xaa = unknown amino acid"
 XX
 PN WO9640933-A1.
 XX
 XX 19-DEC-1996.
 PD
 XX
 PF 06-JUN-1996; 96WO-US009209.
 XX
 XX 07-JUN-1995; 95US-00483292.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (UYMA-) UNIV MAHIDOL AT SALAYA.
 PA
 XX Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
 PI Kinney R, Trent DW;

XX
 DR WPI; 1997-052330/05.
 XX P-PSDB; AAW06590.
 XX
 PT PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
 PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
 PT quadravalent vaccine for protecting against Dengue virus infection.
 XX
 XX Claim 23; Page 107-121; 261pp; English.
 XX
 CC This sequence encodes the polyprotein from Dengue 2 virus, strain 16681.
 CC The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, PDK
 CC NS4A, NS4B and NS5 proteins. A clone of this wildtype viral sequence, PDK
 CC -53, may be used in the production of a quadravalent vaccine which
 CC provides immunity against all four serotypes of dengue virus. The vaccine
 CC also comprises a chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or
 CC a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to
 CC protect against infection by all four serotypes of dengue virus, DEN-1,
 CC DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue
 CC haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used
 CC to produce the recombinant protein products of the DNA constructs which
 CC are used in the vaccines. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2255 T; 0 U; 2 Other;
 Query Match 89.3%; Score 25; DB 2; Length 10723;
 Best Local Similarity 89.3%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
 DB 304 CCCATCTCTCAATATCCCTGCTGTGG 277
 RESULT 8
 AAT49304/C
 ID AAT49304 standard; cDNA; 10723 BP.
 XX
 AC AAT49304;
 XX
 DT 27-AUG-2003 (revised)
 DT 12-SEP-1997 (first entry)
 XX
 DE cDNA encoding polyprotein of attenuated DEN-2 virus, PDK-53.
 XX
 KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
 KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
 KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
 KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
 DHF; DSS; ss.
 XX
 OS Dengue virus type 2 (strain 16681).
 XX
 FH Key Location/Qualifiers
 FT mutation 57
 FT /*tag= b
 FT /note= "C>T mutation"
 FT CDS 97..10272
 FT /*tag= a
 FT /product= "DEN-2 attenuated polyprotein
 FT /transl_except(pos:643..645, aa:Xaa)
 FT /transl_except(pos:1135..1137, aa:Xaa)
 FT /transl_except(pos:1393..1395, aa:Xaa)
 FT /transl_except(pos:2809..2811, aa:Xaa)
 FT /transl_except(pos:3040..3042, aa:Xaa)
 FT /transl_except(pos:9208..9210, aa:Xaa)"
 FT /note= "Xaa = unknown amino acid"
 FT mutation 524
 FT /*tag= c
 FT /note= "A>T mutation, causes Asp to Val substitution"
 FT mutation 2055
 FT /*tag= d

```

FT mutation /note= "C>T mutation"
FT 2579 /*tag= e
FT /note= "G>A mutation, causes Gly to Asp substitution"
FT 4018 /*tag= f
FT /note= "C>T mutation, causes Leu to Phe substitution"
FT 5547 /*tag= g
FT /note= "C>T mutation"
FT 6599 /*tag= h
FT /note= "G>C mutation, causes Gly to Ala substitution"
FT 8571 /*tag= i
FT /note= "C>T mutation"
XX
XX WO9640933-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US009209.
XX
XX 07-JUN-1995; 95US-00483292.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
XX Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
XX Kinney R, Trent DW;
XX WPI; 1997-052330/05.
XX P-PSDB; AAW06591.
XX
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
XX also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
XX quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Claim 27; Page 122-136; 261pp; English.
XX
XX This sequence encodes the polypeptide from an attenuated derivative of
XX Dengue 2 virus, strain 16681. The derivative is designated PDK-53. The
XX polypeptide comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A,
XX NS4B and NS5 proteins. The PDK-53 viral sequence may be used in the
XX production of a quadravalent vaccine which provides immunity against all
XX four serotypes of dengue virus. The vaccine also comprises a chimeric DEN
XX -2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus.
XX The new quadravalent vaccines are used to protect against infection by
XX all four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and DEN-4, which
XX can lead to dengue fever or fatal dengue haemorrhagic fever/dengue shock
XX syndrome (DHF/DSS). Host cells are used to produce the recombinant
XX protein products of the DNA constructs which are used in the vaccines.
XX (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 10723 BP; 3548 A; 2196 C; 2711 G; 2261 T; 0 U; 7 Other;
Query Match 89.3%; Score 25; DB 2; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCMTCAANNATCCCTGCTGTGG 28
| | | | | | | | | | | | | | | | | |
Db 304 CCCATCTCTTCAATATCCCTGCTGTGG 277

RESULT 9
AAD14614/c
ID AAD14614 standard; cDNA; 10723 BP.
XX
XX AAD14614;
XX
XX 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX

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```

XX Dengue virus (DEN)-2/1-VP1 chimeric cDNA.
XX
XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
XX immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
XX Dengue virus; type I.
XX Dengue virus; type II.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 97..10722
XX /*tag= a
XX /product= "DEN-2/1-VP1 fusion protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07993.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 5; Page 422-438; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes dengue virus (DEN)-2/1-VP1 fusion protein related to the
XX invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
XX comprising a valine at the non-structural protein (NS3)-250 and the
XX premembrane/membrane protein (prM) and an envelope protein (E) from wild-
XX type DEN-1 16007 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 10723 BP; 3522 A; 2218 C; 2725 G; 2258 T; 0 U; 0 Other;
Query Match 89.3%; Score 25; DB 4; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCMTCAANNATCCCTGCTGTGG 28
| | | | | | | | | | | | | | | | | |
Db 304 CCCATCTCTTCAATATCCCTGCTGTGG 277

RESULT 10
AAD14607/c
ID AAD14607 standard; cDNA; 10723 BP.
XX
XX AAD14607;
XX
XX 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX

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DE Wild-type, virulent DEN-2 16681 CDNA.
XX
KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal;
KW avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX
OS Dengue virus; type II.
XX
FH Key Location/Qualifiers
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2 16681 protein"
XX
PN WO200160847-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
DR WPI: 2001-497162/54.
DR P-PSDB; AAE07986.
XX
PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 3; Page 252-268; 470pp; English.
XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present CDNA
CC sequence encodes wild-type, virulent dengue-2 (DEN-2) 16681 virus protein
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, premembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2257 T; 0 U; 0 Other;
Query Match 89.3%; Score 25; DB 4; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTGTCANNATCCCTGCTGTGG 28
Db 304 CCCATCTGTCANNATCCCTGCTGTGG 277

RESULT 11
AAD14606/c
ID AAD14606 standard; cDNA; 10723 BP.
XX
AC AAD14606;
XX
DT 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX

DE Wild-type, virulent DEN-2 16681 chimeric CDNA.
XX
KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
OS Dengue virus; type II.
XX
OS Dengue virus; type IV.
XX
CH Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2/4-VP1 fusion protein"
XX
PN WO200160847-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
DR WPI: 2001-497162/54.
DR P-PSDB; AAE07985.
XX
PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 3; Page 227-243; 470pp; English.
XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present CDNA
CC sequence encodes wild-type, virulent dengue-2 (DEN-2) 16681 virus protein
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, premembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10723 BP; 3493 A; 2186 C; 2752 G; 2292 T; 0 U; 0 Other;
Query Match 89.3%; Score 25; DB 4; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTGTCANNATCCCTGCTGTGG 28
Db 304 CCCATCTGTCANNATCCCTGCTGTGG 277

RESULT 12
AAD14608/c
ID AAD14608 standard; cDNA; 10723 BP.
XX
AC AAD14608;
XX
DT 01-NOV-2001 (first entry)
DT Attenuated, vaccine-strain DEN-2 PDK-53 variant CDNA.
XX

```

KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal; muten;
KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
KW ss.

XX Dengue virus; type II.

OS Synthetic.

XX Key Location/Qualifiers

FT mutation replace(57, C)

FT mutation /*tag= b

FT CDS 97..10272

FT /*tag= a

FT /product= "DEN-2 PDK-53 protein variant"

FT mutation replace(524, A)

FT /*tag= C

FT mutation replace(2055, C)

FT /*tag= d

FT mutation replace(2579, G)

FT /*tag= e

FT mutation replace(4018, C)

FT /*tag= f

FT mutation replace(5270, A)

FT /*tag= g

FT mutation replace(5547, T)

FT /*tag= h

FT mutation replace(6599, G)

FT /*tag= i

FT mutation replace(8571, C)

FT /*tag= j

XX WO200160847-A2.

PN

XX

XX

XX

XX 16-FEB-2001; 2001WO-US005142.

XX 16-FEB-2000; 2000US-0182829P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;

XX WPI; 2001-497162/54.

XX P-PSDB; AAE07987.

XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.

XX Example 1; Page 276-292; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes attenuated dengue-2 (DEN-2) PDK-53 virus protein variant
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, premembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region

XX Sequence 10723 BP; 3552 A; 2198 C; 2711 G; 2262 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 4; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTTGG 28

DB 304 CCCATCTCTTCATATCCCTGCTGTTGG 277

RESULT 13

AAD14609/c

ID AAD14609 standard; cDNA; 10756 BP.

XX AAD14609;

XX

DT 11-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 01-NOV-2001 (first entry)

XX

DE Dengue virus (DEN) -2/WN-PPI chimeric cDNA.

XX

XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;

XX immunogenic; viral disease; pharmaceutical; chimeric; ss.

XX

OS Dengue virus; type II.

OS West Nile virus.

OS Chimeric.

XX

FT Key Location/Qualifiers

FT CDS 97..10305

FT /*tag= a

FT /product= "DEN-2/WN-PPI fusion protein"

XX

XX WO200160847-A2.

XX

XX

XX 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US005142.

XX 16-FEB-2000; 2000US-0182829P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;

XX WPI; 2001-497162/54.

XX P-PSDB; AAE07988.

XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.

XX Example 6; Page 300-316; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN) -2/WN-PPI fusion protein related to
CC the invention. This fusion protein contains DEN-2 16681 backbone and the
CC premembrane/membrane protein (prM) and an envelope protein (E) from West
CC Nile NY99. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-
CC SEP-2003 to standardise OS field)

XX Sequence 10756 BP; 3422 A; 2254 C; 2788 G; 2292 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 4; Length 10756;
Best Local Similarity 89.3%; Pred. No. 0.37;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
304 CCCATCTCTCANNATCCCTGCTGTGG 277

RESULT 14

AAT75919/c

ID AAT75919 standard; DNA; 32 BP.

XX AC AAT75919;

XX DT 15-SEP-1997 (first entry)

XX DE DEN-2 cloning/sequencing sense primer, D2-274.

XX KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;

XX KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;

XX KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;

XX KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;

XX KW DHF; DSS; PCR; amplify; polymerase chain reaction; primer; ss.

XX OS Synthetic.

XX PN WO9640933-A1.

XX PD 19-DEC-1996.

XX PF 06-JUN-1996; 96WO-US009209.

XX PR 07-JUN-1995; 95US-00483292.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PA (UYNA-) UNIV MAHIDOL AT SALAYA.

XX PI Bhamarapavati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;

XX PI Kinney R, Trent DW;

XX PI WPI; 1997-052330/05.

XX PT PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -

XX PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a

XX PT quadravalent vaccine for protecting against Dengue virus infection.

XX PS Example; Page 100; 261pp; English.

XX CC The sequences given in AAT75909-T76029 are primers which were used in the

XX CC amplification, cloning and sequencing of the Dengue-2 viral cDNA's of the

XX CC invention. The Dengue 2 viral DNA encodes a polyprotein which comprises

XX CC the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5 proteins.

XX CC The quadravalent vaccine of the invention comprises an attenuated Dengue

XX CC virus clone, PDK-53, and a chimeric DEN-2/1 virus, a chimeric DEN-2/3

XX CC virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are

XX CC used to protect against infection by all four serotypes of dengue virus,

XX CC DEN-1, DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal

XX CC dengue haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are

XX CC used to produce the recombinant protein products of the DNA constructs

XX CC which are used in the vaccines

XX SQ Sequence 32 BP; 12 A; 7 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 83.6%; Score 23.4; DB 2; Length 32;
Best Local Similarity 85.7%; Pred. No. 0.74;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
31 CCCATCTCTCAGTATCCCTGCTGTGG 4

RESULT 15
AAD14612/c
ID AAD14612 standard; cDNA; 10648 BP.

XX AC AAD14612;

XX DT 11-SEP-2003 (revised)

XX DT 01-NOV-2001 (first entry)

XX DE Wild-type, virulent DEN-4 1036 cDNA.

XX KW Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal;

XX KW avirulent; immunogenic; viral disease; pharmaceutical; ss.

XX OS Dengue virus; type IV.

XX FH Key Location/Qualifiers

XX FT 102..10265

XX FT /*tag= a

XX FT /product= "DEN-4 1036 protein"

XX PN WO200160847-A2.

XX PD 23-AUG-2001.

XX PF 16-FEB-2001; 2001WO-US005142.

XX PR 16-FEB-2000; 2000US-0182829P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapavati N;

XX PI WPI; 2001-497162/54.

XX PR P-PSDB; AAE07991.

XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for

XX PT vaccinating against a range of dengue viruses.

XX PS Example 3; Page 373-389; 470pp; English.

XX CC The invention relates to avirulent, immunogenic flavivirus chimeras

XX CC comprising amino acid mutations in the non-structural proteins of a

XX CC flavivirus. Chimeric viruses containing the attenuation-mutated non-

XX CC structural genes of the virus are used as a backbone into which the

XX CC structural protein genes of a second flavivirus strain are inserted.

XX CC These chimeric viruses elicit pronounced immunogenicity but lack the

XX CC accompanying clinical symptoms of viral disease. Attenuated chimeric

XX CC flaviviruses are combined in a pharmaceutical composition to confer

XX CC simultaneous immunity against several strains of pathogenic flaviviruses

XX CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic

XX CC flavivirus chimeras are also used as immunogens or multivalent vaccines

XX CC to confer simultaneous protection against infections. The present cDNA

XX CC sequence encodes wild-type, virulent dengue-4 (DEN-4) 1036 virus protein

XX CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1

XX CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome

XX CC contains 5' non-coding region followed by a capsid protein (C) encoding

XX CC region, premembrane/membrane protein (prM) encoding region, an envelope

XX CC protein (E) encoding region, followed by the region encoding non-

XX CC structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'

XX CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)

XX SQ Sequence 10648 BP; 3294 A; 2213 C; 2810 G; 2331 T; 0 U; 0 Other;

Query Match 83.6%; Score 23.4; DB 4; Length 10648;
Best Local Similarity 85.7%; Pred. No. 1.9;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
306 CCCATCTTTTCAGATCCCTGCTGTGG 279

Search completed: August 3, 2004, 18:46:01
Job time : 155.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 18:28:49 ; Search time 37 Seconds
(without alignments)
419.963 Million cell updates/sec

Title: US-10-085-944-1

Perfect score: 28

Sequence: 1 cccatctcannatccctgtgttg 28

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/prodata/2/ina/5B-COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A-COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B-COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS-COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	21.8	77.9	3381	3	US-08-937-195-1
C 3	21.8	77.9	3381	3	US-08-937-195-2
C 4	21.8	77.9	3381	3	US-08-915-152-1
C 5	21.8	77.9	3381	3	US-08-915-152-2
C 6	21.8	77.9	3381	5	PCT-US96-07627-1
C 7	21.8	77.9	3381	5	PCT-US96-07627-2
C 8	20.2	72.1	10718	3	US-08-325-425B-1
C 9	18.8	67.1	5674	1	US-07-807-043B-8
C 10	18.8	67.1	5674	1	US-08-190-411A-1
C 11	18.8	67.1	5674	1	US-08-299-849B-8
C 12	18.8	67.1	5674	2	US-08-560-024-1
C 13	18.8	67.1	5674	2	US-08-142-368A-8
C 14	18.8	67.1	5674	3	US-08-967-727-8
C 15	18.8	67.1	5674	3	US-08-037-230D-8
C 16	18.8	67.1	5674	4	US-09-583-850-8
C 17	18.8	67.1	5674	4	US-09-579-197-8
C 18	18.8	67.1	5674	4	US-09-404-026-8
C 19	18.8	67.1	5674	4	US-09-312-464-8
C 20	18.8	67.1	5707	2	US-08-472-809B-8
C 21	18.8	67.1	6345	2	US-08-472-809B-7
C 22	18.2	65.0	2917	2	US-08-437-607A-3
C 23	18.2	65.0	3030	4	US-09-439-313-333
C 24	18.2	65.0	3030	4	US-09-352-616A-333
C 25	18.2	65.0	3030	4	US-09-232-149A-333
C 26	18.2	65.0	3030	4	US-09-636-213-333
C 27	18.2	65.0	3030	4	US-09-685-166A-333

C 28	18.2	65.0	3030	4	US-09-688-489-333	Sequence 333, App
C 29	18.2	65.0	1664976	4	US-08-916-421B-1	Sequence 1, Appli
C 30	17.6	62.9	1064	2	US-08-529-878B-40	Sequence 40, Appl
C 31	17.6	62.9	1514	4	US-09-023-655-1316	Sequence 1316, Ap
C 32	17.6	62.9	2238	1	US-08-389-668A-1	Sequence 1, Appli
C 33	17.6	62.9	2238	1	US-08-732-506-1	Sequence 1, Appli
C 34	17.6	62.9	2238	5	PCT-US95-05768-1	Sequence 1, Appli
C 35	17.6	62.9	19025	4	US-09-849-334-3	Sequence 3, Appli
C 36	17.6	62.9	19025	4	US-10-274-878-3	Sequence 3, Appli
C 37	17.6	62.9	31960	4	US-09-453-702B-11	Sequence 11, Appl
C 38	17.2	61.4	1310	4	US-09-976-594-926	Sequence 926, App
C 39	17.2	61.4	5410	4	US-09-561-818A-7	Sequence 7, Appli
C 40	17.2	61.4	5498	4	US-09-561-818A-5	Sequence 5, Appli
C 41	17.2	61.4	5942	4	US-09-561-818A-3	Sequence 3, Appli
C 42	17.2	61.4	6204	4	US-09-561-818A-1	Sequence 1, Appli
C 43	17	60.7	1867	4	US-09-976-594-631	Sequence 631, App
C 44	17	60.7	4629	2	US-08-484-891-7	Sequence 7, Appli
C 45	17	60.7	4629	4	US-09-150-811-7	GENERAL INFORMA

ALIGNMENTS

RESULT 1
US-08-869-423-1/c
; Sequence 1, Application US/08869423
; Patent No. 6455509
; GENERAL INFORMATION:
; APPLICANT: Kochel, Tadeusz
; APPLICANT: Porter, Kevin R.
; APPLICANT: Raviprakash, Kanakatte
; APPLICANT: Hoffman, Stephen L.
; APPLICANT: Hayes, Curtis G.
; TITLE OF INVENTION: Dengue Nucleic Acid Vaccines that Induce
; TITLE OF INVENTION: Neutralizing Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Naval Medical Res. & Dev. Cmd.
; STREET: 8901 Wisconsin Ave., Bldg. 1, T-12
; CITY: Bethesda
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20889-5606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,423
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,839
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kalish, Daniel
; REGISTRATION NUMBER: 33,599
; REFERENCE/DOCKET NUMBER: NC 77,654
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 295-5642
; TELEFAX: (301) 295-1022
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:

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/ ORGANISM: Dengue virus
/ STRAIN: New Guinea C
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT: Prem and Envelope
/ MAP POSITION: 330-2446
/ UNITS: bp
/ PUBLICATION INFORMATION:
/ AUTHORS: Gruenberg, A
/ AUTHORS: Woo, W S
/ AUTHORS: Biedrzycka, A
/ AUTHORS: Wright, P J
/ TITLE: Partial nucleotide sequence and deduced amino
/ TITLE: acid sequence of the structural proteins of dengue
/ TITLE: virus type 2, New Guinea C and PUO-218 strains
/ JOURNAL: J. Gen. Virol.
/ VOLUME: 69
/ PAGES: 1391-1398
/ DATE: 1988
/ PUBLICATION INFORMATION:
/ AUTHORS: Irie, K
/ AUTHORS: Mohan, P M
/ AUTHORS: Sasaguri, Y
/ AUTHORS: Putnak, R
/ AUTHORS: Padmanabhan, R
/ TITLE: Sequence Analysis of Cloned dengue virus type
/ TITLE: 2 genome (New Guinea-C strain)
/ JOURNAL: Gene
/ VOLUME: 75
/ ISSUE: 2
/ PAGES: 197-211
/ DATE: 1989
/ PUBLICATION INFORMATION:
/ AUTHORS: Yaegashi, T
/ AUTHORS: Vakharia, V N
/ AUTHORS: Page, K
/ AUTHORS: Sasaguri, Y
/ AUTHORS: Feighny, R
/ AUTHORS: Padmanabhan, R
/ JOURNAL: Gene
/ VOLUME: 46
/ ISSUE: 2-3
/ PAGES: 257-267
/ DATE: 1986
/ US-08-869-423-1

Query Match 89.3%; Score 25; DB 4; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.023;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCNCANNATCCCTGCTTGG 28
Db . 228 CCCATCTTCAGTATCCCTGCTTGG 201

RESULT 2
US-08-937-195-1/c
/ Sequence 1, Application US/08937195
/ Patent No. 6135561
/ GENERAL INFORMATION:
/ APPLICANT: IVY, JOHN M.
/ APPLICANT: KAKANO, EILEEN
/ APPLICANT: CLEMENTS, DAVID
/ TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORRISON & FOERSTER
/ STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
/ CITY: WASHINGTON
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20006-1012
/ COMPUTER READABLE FORM:
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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/937,195
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA: US 08/488,807
/ APPLICATION NUMBER: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MURASHIGE, KATE H.
/ REGISTRATION NUMBER: 29,959
/ REFERENCE/DOCKET NUMBER: 4733-0003.20
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-1500
/ TELEFAX: (202) 887-0763
/ TELEX: 90-4030
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3381 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ ORIGINAL SOURCE:
/ ORGANISM: Dengue virus
/ STRAIN: Serotype 2 (Den-2)
/ IMMEDIATE SOURCE:
/ CLONE: Den-2 PRI59/S1
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: Group(103, 1940, 1991, 2025)
/ OTHER INFORMATION: /note= "Positions in the S1 strain
/ OTHER INFORMATION: representing corrections to the wild type DEN-2 PRI59 strain"
/ OTHER INFORMATION: reported by Hahn(Citation #1)"
/ OTHER INFORMATION: /citation= ([1])
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1218
/ OTHER INFORMATION: /note= "G is replaced by A for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1260
/ OTHER INFORMATION: /note= "T is replaced by G for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1762
/ OTHER INFORMATION: /note= "G is replaced by A for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1929
/ OTHER INFORMATION: /note= "C is replaced by T for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 2310
/ OTHER INFORMATION: /note= "A is replaced by N for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence for Capsid."
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 343
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence for preMembrane"
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Membrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Envelope"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
PAGES: 167-180
DATE: 1988
US-08-937-195-1

Query Match 77.9%; Score 21.8; DB 3; Length 3381;
Best Local Similarity 82.1%; Pred. No. 0.75;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCCTCANNATCCCTGCTGTTGG 28
|||||
Db 208 CCCACTTTTAAATATCCCTGCTGTTGG 181

RESULT 3
US-08-937-195-2/c
Sequence 2, Application US/08937195
Patent No. 6136561
GENERAL INFORMATION:
APPLICANT: IVI, JOHN M.
APPLICANT: KAKANO, EILEEN
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FORSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,195
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,807
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (DEN-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3381
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1216..1218
OTHER INFORMATION: /note= "GAG(coding for Glu) is
OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR159;
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= (11)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1258..1260
OTHER INFORMATION: /note= "GTG(coding for Val) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159;
OTHER INFORMATION: Strain(Citation #1)"
OTHER INFORMATION: /citation= (11)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1762..1764
OTHER INFORMATION: /note= "ATT(coding for Ile) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159;
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= (11)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1927..1929
OTHER INFORMATION: /note= "AGT(Coding for Ser) is
OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159;
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= (11)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Capsid"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 343
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for preMembrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Membrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Envelope"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
PAGES: 167-180
DATE: 1988
US-08-937-195-2

Query Match 77.9%; Score 21.8; DB 3; Length 3381;
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Best Local Similarity 82.1%; Pred. No. 0.75;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 208 CCCATCTTTTAAATATCCCTGCTGTGG 181

RESULT 4
US-08-915-152-1/c
; Sequence 1, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,152
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,469
; FILING DATE: 10-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: group(103, 1940, 1991, 2025)
; OTHER INFORMATION: /note= "Positions in the S1 strain
; OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
; OTHER INFORMATION: reported by Hahn(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1218
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1260
; OTHER INFORMATION: /note= "T is replaced by G for
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; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1929
; OTHER INFORMATION: /note= "C is replaced by T for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2310
; OTHER INFORMATION: /note= "A is replaced by N for
; OTHER INFORMATION: Wild-Type sequence"
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; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; US-08-915-152-1

Query Match 77.9%; Score 21.8; DB 3; Length 3381;
Best Local Similarity 82.1%; Pred. No. 0.75;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 208 CCCATCTTTTAAATATCCCTGCTGTGG 181

RESULT 5
US-08-915-152-2/c
; Sequence 2, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
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/ COUNTRY: USA
/ ZIP: 20006-1812
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/915,152
/ FILING DATE: 20-AUG-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION: 435
/ APPLICATION NUMBER: US 08/500,469
/ FILING DATE: 10-JUL-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MURASHIGE, KATE H.
/ REGISTRATION NUMBER: 29,959
/ REFERENCE/DOCKET NUMBER: 4733-0003.21
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-1500
/ TELEFAX: (202) 887-0763
/ TELEX: 90-4030
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3381 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ ORIGINAL SOURCE:
/ ORGANISM: Dengue virus
/ STRAIN: Serotype 2 (DEN-2)
/ IMMEDIATE SOURCE:
/ CLONE: Den-2 PR159/S1
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..3381
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1216..1218
/ OTHER INFORMATION: /note= "GAG(coding for Glu) is
/ OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR15
/ OTHER INFORMATION: strain(Citation #1)"
/ OTHER INFORMATION: /citation= ([1])
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1258..1260
/ OTHER INFORMATION: /note= "GTG(coding for Val) is
/ OTHER INFORMATION: replaced for GTT(coding for Val) for the wild-type DEN-2 PR15
/ OTHER INFORMATION: Strain(Citation #1)"
/ OTHER INFORMATION: /citation= ([1])
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1762..1764
/ OTHER INFORMATION: /note= "ATT(coding for Ile) is
/ OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
/ OTHER INFORMATION: strain(Citation #1)"
/ OTHER INFORMATION: /citation= ([1])
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1927..1929
/ OTHER INFORMATION: /note= "AGT(Coding for Ser) is
/ OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
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/ OTHER INFORMATION: /citation= ([1])
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1
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/ OTHER INFORMATION: sequence for Capsid"
/ FEATURE:
/ NAME/KEY: misc_feature
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/ OTHER INFORMATION: /note= "G is replaced by A for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ OTHER INFORMATION: /note= "Start of coding strand
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/ OTHER INFORMATION: sequence of Membrane"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 841
/ OTHER INFORMATION: /note= "Start of coding strand
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 2326
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence for NS1"
/ PUBLICATION INFORMATION:
/ AUTHORS: Hahn, Y.S.
/ JOURNAL: Virology
/ VOLUME: 162
/ PAGES: 167-180
/ DATE: 1988
/ US-08-915-152-2
/ Query Match 77.9%; Score 21.8; DB 3; Length 3381;
/ Best Local Similarity 82.1%; Pred. No. 0.75;
/ Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
/ QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
/ Db 208 CCCATCTTTTAATATCCCTGCTGTGG 181
/ RESULT 6
/ PCT-US96-07627-1/c
/ Sequence 1, Application PC/TUS9607627
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
/ NUMBER OF SEQUENCES: 50
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/07627
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3381 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ ORIGINAL SOURCE:
/ ORGANISM: Dengue virus
/ STRAIN: Serotype 2 (Den-2)
/ IMMEDIATE SOURCE:
/ CLONE: Den-2 PR159/S1
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: group(103, 1940, 1991, 2025)
/ OTHER INFORMATION: /note= "Positions in the S1 strain
/ OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
/ OTHER INFORMATION: reported by Hahn(Citation #1)"
/ OTHER INFORMATION: /citation= ([1])
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1218
/ OTHER INFORMATION: /note= "G is replaced by A for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
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/ NAME/KEY: misc_feature
/ LOCATION: 1260_ /note= "T is replaced by G for
/ OTHER INFORMATION: Wild-Type sequence"
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/ NAME/KEY: misc_feature
/ LOCATION: 1762_ /note= "G is replaced by A for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1929_ /note= "C is replaced by T for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 2310_ /note= "A is replaced by N for
/ OTHER INFORMATION: Wild-Type sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1_ /note= "Start of coding strand
/ OTHER INFORMATION: sequence for Capsid."
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 343_ /note= "Start of coding strand
/ OTHER INFORMATION: sequence for preMembrane"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 616_ /note= "Start of coding strand
/ OTHER INFORMATION: sequence for Membrane"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 841_ /note= "Start of coding strand
/ OTHER INFORMATION: sequence for Envelope"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 2326_ /note= "Start of coding strand
/ OTHER INFORMATION: sequence for NS1"
/ PUBLICATION INFORMATION:
/ AUTHORS: Hahn, Y.S.
/ JOURNAL: Virology
/ VOLUME: 162
/ PAGES: 167-180
/ DATE: 1988
PCT-US96-07627-1
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Query Match 77.9%; Score 21.8; DB 5; Length 3381;
Best Local Similarity 82.1%; Pred. No. 0.75;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 CCCATCTCNCANNATCCCTGCTGTGG 28
Db 208 CCCATCTTTTATATATCCCTGCTGTGG 181
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RESULT 7
PCT-US96-07627-2/c
/ Sequence 2, Application PC/TUS9607627
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
/ NUMBER OF SEQUENCES: 50
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/07627
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3381 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ ORIGINAL SOURCE:
/ ORGANISM: Dengue virus
/ STRAIN: Serotype 2(DEN-2)
/ IMMEDIATE SOURCE:
/ CLONE: Den-2 PR159/S1
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..3381
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1216_..1218
/ OTHER INFORMATION: /note= "GAG(coding for Glu) is
/ OTHER INFORMATION: replaced by GAA(coding for Val) for the wild-type DEN-2 PR15;
/ OTHER INFORMATION: strain(Citation #1)"
/ OTHER INFORMATION: /citation= ([1])
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1258_..1260
/ OTHER INFORMATION: /note= "GTG(coding for Val) is
/ OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR15;
/ OTHER INFORMATION: strain(Citation #1)"
/ OTHER INFORMATION: /citation= ([1])
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1762_..1764
/ OTHER INFORMATION: /note= "ATT(coding for Ile) is
/ OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
/ OTHER INFORMATION: strain(Citation #1)"
/ OTHER INFORMATION: /citation= ([1])
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1927_..1929
/ OTHER INFORMATION: /note= "AGT(Coding for Ser) is
/ OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
/ OTHER INFORMATION: strain(Citation #1)"
/ OTHER INFORMATION: /citation= ([1])
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1_
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence for Capsid"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 343_
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence for preMembrane"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 616_
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence of Membrane"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 841_
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence of Envelope"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 2326_
/ OTHER INFORMATION: /note= "Start of coding strand
/ OTHER INFORMATION: sequence for NS1"
/ PUBLICATION INFORMATION:
/ AUTHORS: Hahn, Y.S.
/ JOURNAL: Virology
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/ VOLUME: 162
/ PAGES: 167-180
/ DATE: 1988
/ PCT-US96-07627-2
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/ Query Match 77.9%; Score 21.8; DB 5; Length 3381;
/ Best Local Similarity 82.1%; Pred. No. 0.75;
/ Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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/ QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
/ ||||| ||||| ||||| ||||| |||||
/ Db 208 CCCATCTTTTAATAATCCCTGCTGTGG 181
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/ RESULT 8
/ US-08-325-426B-1/c
/ Sequence 1, Application US/08325426B
/ Patent No. 6017535
/ GENERAL INFORMATION:
/ APPLICANT: FU, Jianlin
/ APPLICANT: TAN, Boon-Haun
/ APPLICANT: YAP, Eu-Hian
/ APPLICANT: CHAN, Yow-Cheong
/ APPLICANT: TAN, Yin-Hwee
/ TITLE OF INVENTION: CDNA SEQUENCE OF DENGUE VIRUS SEROTYPE 1
/ TITLE OF INVENTION: (SINGAPORE STRAIN)
/ NUMBER OF SEQUENCES: 25
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NIXON and VANDERHVE PC
/ STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
/ CITY: ARLINGTON
/ STATE: VIRGINIA
/ COUNTRY: USA
/ ZIP: 22201-4714
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/325,426B
/ FILING DATE: 16-DEC-1994
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10718 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: CDNA sequence corresponding to
/ MOLECULE TYPE: the genomic RNA of DEN1-8275/90
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Dengue Fever Virus Type 1
/ STRAIN: S275/90
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 81..10268
/ US-08-325-426B-1
/
/ Query Match 72.1%; Score 20.2; DB 3; Length 10718;
/ Best Local Similarity 78.6%; Pred. No. 5.3;
/ Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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/ QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
/ ||||| ||||| ||||| ||||| |||||
/ Db 288 CCCATCTAGCCAAATTCCTGCTGTGG 261
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/ RESULT 9
/ US-07-807-043B-8
/ Sequence 8, Application US/07807043B
/ Patent No. 5342774
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/ GENERAL INFORMATION:
/ APPLICANT: Boon, Thierry, Van den Eynde, Beno t
/ TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
/ TITLE OF INVENTION: Rejection Antigens and Uses Thereof
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Felfe & Lynch
/ STREET: 805 Third Avenue
/ CITY: New York City
/ STATE: New York
/ ZIP: 10022
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
/ COMPUTER: IBM
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: Wordperfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/807,043B
/ FILING DATE: 19911212
/ CLASSIFICATION: 424
/ PRIOR APPLICATION NUMBER: 07/764,364
/ FILING DATE: 23-SEPTEMBER-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/728,838
/ FILING DATE: 9-JULY-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/705,702
/ FILING DATE: 23-May-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hanson, No. 5342774man D.
/ REGISTRATION NUMBER: 30,946
/ REFERENCE/DOCKET NUMBER: LUD 253.3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 688-9200
/ TELEFAX: (212) 838-3884
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5674 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: singular
/ TOPOLOGY: linear
/ MOLECULE TYPE: genomic DNA
/ FEATURE:
/ NAME/KEY: MAGE-1 gene
/ US-07-807-043B-8
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/ Query Match 67.1%; Score 18.8; DB 1; Length 5674;
/ Best Local Similarity 80.0%; Pred. No. 20;
/ Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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/ QY 1 CCCATCTCTCANNATCCCTGCTGT 25
/ ||||| ||||| ||||| ||||| |||||
/ Db 1897 CTCATCTTGTTCAGATCCCTGCTGT 1921
/
/ RESULT 10
/ US-08-190-411A-1
/ Sequence 1, Application US/08190411A
/ Patent No. 5541104
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Yao-Tseng; Stockert, Elisabeth;
/ APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
/ APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;
/ APPLICANT: Old, Lloyd J.
/ TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO
/ TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1,
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Felfe & Lynch
/ STREET: 805 Third Avenue
/ CITY: New York City
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STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,411A
FILING DATE: 01-FEBRUARY-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5541104man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5354
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5674 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
FEATURE:
NAME/KEY: MAGE-1 gene
US-08-190-411A-1

Query Match 67.1%; Score 18.8; DB 1; Length 5674;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGAAATCCCTGCTGT 1921

RESULT 11
US-08-299-849B-8
Sequence 8, Application US/08299849B
Patent No. 5612201
GENERAL INFORMATION:
APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
APPLICANT: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,849B
FILING DATE: 1-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5612201man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5355
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5674 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
FEATURE:
NAME/KEY: MAGE-1 gene
US-08-299-849B-8

Query Match 67.1%; Score 18.8; DB 1; Length 5674;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGAAATCCCTGCTGT 1921

RESULT 12
US-08-560-024-1
Sequence 1, Application US/08560024
Patent No. 5843448
GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tsang; Stockert, Elisabeth;
APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1,
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1,
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,024
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
FILING DATE: 01-FEBRUARY-1994
APPLICATION NUMBER: 037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
FILING DATE: 22-MAY-1992
APPLICATION NUMBER: PCT/US92/04354
PRIOR APPLICATION DATA:
FILING DATE: 07/807,043
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
FILING DATE: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION DATA:
FILING DATE: 07/705,702
APPLICATION NUMBER: 07/705,702
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5843448man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5354
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5674 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
FEATURE:
NAME/KEY: MAGE-1 gene
US-08-560-024-1

Query Match 67.1%; Score 18.8; DB 2; Length 5674;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCCTCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGATCCCTGCTGT 1921

RESULT 13
US-08-142-368A-8
Sequence 8, Application US/08142368A
Patent No. 5925729
GENERAL INFORMATION:
APPLICANT: Boon-Falleur, Thierry; Van den Bruggen, Thierry;
APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: 22-MAY-1992
APPLICATION NUMBER: PCT/US92/04354
PRIOR APPLICATION DATA:
FILING DATE: 07/807,043
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
FILING DATE: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION DATA:
FILING DATE: 07/705,702
APPLICATION NUMBER: 07/705,702
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5925729man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5674 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
FEATURE:
NAME/KEY: MAGE-1 gene
US-08-142-368A-8

Query Match 67.1%; Score 18.8; DB 2; Length 5674;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCCTCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGATCCCTGCTGT 1921

RESULT 14
US-08-967-727-8
Sequence 8, Application US/08967727
Patent No. 6025474
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
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RESULT 15
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; Sequence 8, Application US/08037230D
; Patent No. 6235525
; GENERAL INFORMATION:
; APPLICANT: Gauglier, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/037,230D
; FILING DATE: 26-MARCH-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 18:40:54 ; Search time 158 Seconds
(without alignments)
868.911 Million cell updates/sec

Title: US-10-085-944-1

Perfect score: 28

Sequence: 1 cccatctcctcannatccctgtgtgg 28

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Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	21.8	77.9	3381	15	US-10-247-960-2
3	19.2	68.6	691	13	US-10-027-632-281617
4	19.2	68.6	691	16	US-10-027-632-281617
5	18.8	67.1	2739	17	US-10-437-963-62174
6	18.6	66.4	482	15	US-10-029-386-27304
7	18.6	66.4	486	9	US-09-864-761-27448
8	18.6	66.4	577	15	US-10-029-386-13604
9	18.6	66.4	2301	17	US-10-437-963-53513
10	18.6	66.4	6412	17	US-10-322-281-483
11	18.6	66.4	61396	17	US-10-322-281-483
12	18.6	66.4	98634	13	US-10-087-192-1870
13	18.2	65.0	476	10	US-09-814-353-1708
14	18.2	65.0	476	10	US-09-814-353-8061

15	18.2	65.0	1506	13	US-10-027-632-256653	Sequence 256653,
16	18.2	65.0	1506	16	US-10-027-632-256653	Sequence 256653,
17	18.2	65.0	3030	9	US-09-759-143-333	Sequence 333, App
18	18.2	65.0	3030	9	US-09-780-669-333	Sequence 333, App
19	18.2	65.0	3030	9	US-09-822-827-333	Sequence 333, App
20	18.2	65.0	3030	9	US-09-232-880-333	Sequence 333, App
21	18.2	65.0	3030	9	US-09-895-793-333	Sequence 333, App
22	18.2	65.0	3030	9	US-09-895-814-333	Sequence 333, App
23	18.2	65.0	3030	14	US-10-012-896-333	Sequence 333, App
24	18.2	65.0	3030	15	US-10-010-940-333	Sequence 333, App
25	18.2	65.0	3030	15	US-10-144-678A-333	Sequence 333, App
26	18.2	65.0	3030	15	US-10-294-025-333	Sequence 333, App
27	18.2	65.0	77777	17	US-10-318-389-4	Sequence 4, Appli
28	18.2	65.0	81826	15	US-10-175-523-197	Sequence 197, App
29	17.8	63.6	415	13	US-10-027-632-183225	Sequence 183225,
30	17.8	63.6	415	16	US-10-027-632-183225	Sequence 183225,
31	17.8	63.6	1277	17	US-10-437-963-83170	Sequence 83170, A
32	17.8	63.6	90798	17	US-10-318-819A-4	Sequence 4, Appli
33	17.6	62.9	239	9	US-09-864-761-26181	Sequence 26181, A
34	17.6	62.9	353	11	US-09-864-408A-2719	Sequence 2719, Ap
35	17.6	62.9	371	17	US-10-437-963-13942	Sequence 13942, A
36	17.6	62.9	410	9	US-09-864-761-21296	Sequence 21296, A
37	17.6	62.9	453	10	US-09-918-995-14536	Sequence 14536, A
38	17.6	62.9	494	9	US-09-864-761-4549	Sequence 4549, Ap
39	17.6	62.9	566	9	US-09-864-761-9825	Sequence 9825, Ap
40	17.6	62.9	649	13	US-10-027-632-275006	Sequence 275006,
41	17.6	62.9	649	16	US-10-027-632-275006	Sequence 275006,
42	17.6	62.9	700	16	US-10-341-961A-7	Sequence 7, Appli
43	17.6	62.9	796	13	US-10-027-632-156282	Sequence 156282,
44	17.6	62.9	796	16	US-10-027-632-156282	Sequence 156282,
45	17.6	62.9	858	13	US-10-424-599-106253	Sequence 106253,

ALIGNMENTS

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RESULT 1
US-10-085-944-1
; Sequence 1, Application US/10085944
; Publication No. US20020155435A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei-Kung
; TITLE OF INVENTION: DETECTION OF DENGUE VIRUS
; FILE REFERENCE: 12563-004001
; CURRENT APPLICATION NUMBER: US/10/085,944
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/272,535
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; NAME/KEY: misc feature
; LOCATION: 9 13,14
; OTHER INFORMATION: n = inosine
US-10-085-944-1

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Query Match 89.3%; Score 25; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1  CCCATCTCCTCANNATCCCTGCTGTGG 28
        |||||
Db       1  CCCATCTCCTCANNATCCCTGCTGTGG 28

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RESULT 2
US-10-247-960-2/c

; Sequence 2, Application US/10247960
; Publication No. US20030175304A1
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
; APPLICANT: Peters, Iain
; APPLICANT: Collier, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; TITLE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
; FILE REFERENCE: 24733-20005.01
; CURRENT APPLICATION NUMBER: US/10/247,960
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/376,463
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3381
; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-10-247-960-2

Query Match 77.9%; Score 21.8; DB 15; Length 3381;
Best Local Similarity 82.1%; Pred. No. 3;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 208 CCCATCTTTTATATATCCCTGCTGTGG 181

RESULT 3
US-10-027-632-281617/c
; Sequence 281617, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281617
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-281617

Query Match 68.6%; Score 19.2; DB 13; Length 691;
Best Local Similarity 77.8%; Pred. No. 42;

Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 27
Db 562 CCCAGCTCTCTCATGTTCCTGCTGTGG 536

RESULT 4
US-10-027-632-281617/c
; Sequence 281617, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281617
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-281617

Query Match 68.6%; Score 19.2; DB 16; Length 691;
Best Local Similarity 77.8%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 27
Db 562 CCCAGCTCTCTCATGTTCCTGCTGTGG 536

RESULT 5
US-10-437-963-62174/c
; Sequence 62174, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 62174
; LENGTH: 2739
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:

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; OTHER INFORMATION: MAP TO CHRI4.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: SWISSPROT HIT: P80192, EVALUATION 1.00e-72
; OTHER INFORMATION: NT HIT: G114749516, EVALUATION 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: AAL60611.1, EVALUATION 5.00e-76
US-10-029-386-13604

Query Match 66.4%; Score 18.6; DB 15; Length 577;
Best Local Similarity 75.0%; Pred. No. 78;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
DB 93 CCCATCTCTCATACTCACTGCTGTGG 120
|||||

RESULT 9
US-10-437-963-53513/c
; Sequence 53513, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 53513
; LENGTH: 2301
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_55706C.1
US-10-437-963-53513

Query Match 66.4%; Score 18.6; DB 17; Length 2301;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
DB 1933-CCCATCTCTCATGATGATGCTGTGG 1906
|||||

RESULT 10
US-10-322-281-484/c
; Sequence 484, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 484
; LENGTH: 6412
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-322-281-484

Query Match 66.4%; Score 18.6; DB 17; Length 6412;
Best Local Similarity 75.0%; Pred. No. 1e+02;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
DB 1558 CCCATCTCTCACTCTCCCTGCTGTGG 1531
|||||

RESULT 11
US-10-322-281-483/c
; Sequence 483, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 483
; LENGTH: 61396
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(61396)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-483

Query Match 66.4%; Score 18.6; DB 17; Length 61396;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
DB 46542 CCCATCTCTCACTCTCCCTGCTGTGG 46515
|||||

RESULT 12
US-10-087-192-1870/c
; Sequence 1870, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1870
; LENGTH: 98634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-1870

Query Match 66.4%; Score 18.6; DB 13; Length 98634;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
DB 18384 CCCATCTCTCACTCACTGCTGTGG 18357
|||||

RESULT 13


```
US-09-814-353-1708/c
; Sequence 1708, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1708
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-1708
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Query Match 65.0%; Score 18.2; DB 10; Length 476;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY 2 CCATCTCCTCANNATCCCTGCTGTTG 27
Db 424 CCTTCTCCTCACAGTCCCTGCTGCTG 399
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```
RESULT 14
US-09-814-353-8061/c
; Sequence 8061, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8061
; LENGTH: 476
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-09-814-353-8061
Query Match 65.0%; Score 18.2; DB 10; Length 476;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CCATCTCCTCANNATCCCTGCTGTTG 27
Db 424 CCTTCTCCTCACAGTCCCTGCTGCTG 399

RESULT 15
US-10-027-632-256653
; Sequence 256653, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256653
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-256653
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Query Match 65.0%; Score 18.2; DB 13; Length 1506;
Best Local Similarity 76.9%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY 3 CATCTCCTCANNATCCCTGCTGTTG 28
Db 293 CATCTCCTCACCAGTCTTGCTGTTG 318
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Search completed: August 3, 2004, 19:57:35
Job time : 160 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 18:26:44 ; Search time 1253 Seconds
(without alignments)
667.311 Million cell updates/sec

Title: US-10-085-944-1

Perfect score: 28
Sequence: 1 cccatctcannatccctgctgttg 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19.2	68.6	287	10	BB338318
2	19.2	68.6	453	28	AQ517624 HS 5140.B
3	19.2	68.6	481	13	BX109154
4	19.2	68.6	577	29	CC690447

5	19.2	68.6	646	14	CD443887
6	19.2	68.6	659	29	AG063981
7	19.2	68.6	938	29	CG232800
8	19.2	68.6	952	29	CG456461
9	19.2	68.6	961	29	CNS06EAJ
10	19.2	68.6	1018	29	CG456420
11	19.2	68.6	1139	28	CC187707
12	19.2	68.6	2314	11	BC028893
13	18.8	67.1	413	10	BF723268
14	18.8	67.1	445	14	CF546284
15	18.8	67.1	463	12	BI048424
16	18.8	67.1	990	29	CNS01L0W
17	18.8	67.1	2185	29	CG755418
18	18.6	66.4	231	10	BF655438
19	18.6	66.4	231	10	BF655439
20	18.6	66.4	239	9	AV361516
21	18.6	66.4	245	13	BX639040
22	18.6	66.4	274	10	BF440266
23	18.6	66.4	280	10	AW354424
24	18.6	66.4	285	9	AV116369
25	18.6	66.4	297	10	BF600952
26	18.6	66.4	300	10	BF174849
27	18.6	66.4	389	10	BF601010
28	18.6	66.4	411	12	BM286538
29	18.6	66.4	413	9	AA068952
30	18.6	66.4	414	9	AI614834
31	18.6	66.4	420	9	AU232945
32	18.6	66.4	421	10	AW477778
33	18.6	66.4	446	14	CD804048
34	18.6	66.4	472	14	CB418067
35	18.6	66.4	503	12	BM090019
36	18.6	66.4	540	9	AV665694
37	18.6	66.4	550	14	CF162479
38	18.6	66.4	568	28	AQ793162
39	18.6	66.4	598	9	AI390262
40	18.6	66.4	602	13	BQ790197
41	18.6	66.4	622	14	CF747473
42	18.6	66.4	625	14	CA371379
43	18.6	66.4	627	28	AZ928229
44	18.6	66.4	677	10	BB478112
45	18.6	66.4	700	12	BI735720

ALIGNMENTS

RESULT 1	BB338318/c	287 bp	linear	EST 11-JUL-2000
LOCUS	BB338318	RIKEN full-length enriched, 10 days neonate cerebellum Mus musculus cDNA clone B930012N10 3', similar to U1352 Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, mRNA sequence.		
DEFINITION	BB338318			
ACCESSION	BB338318			
VERSION	BB338318.1	GI:9047081		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 287)			
	Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Taya, T., Teunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamana, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and			


```

TITLE
JOURNAL
COMMENT
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IMAGp998J044588
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACGGAACAGCTATGAC.

FEATURES
source
Location/Qualifiers
1..481
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998J044588 ; IMAGE:1873635"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Co8"
/note="Organ: Colon; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 68.6%; Score 19.2; DB 13; Length 481;
Best Local Similarity 77.8%; Pred. No. 2.8e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCATCTCTCANNATCCCTGCTGTG 27
|||||
Db 401 CCACCTCCACAGCATCCCGCTGTG 427

RESULT 4
CC690447 577 bp DNA linear GSS 19-JUN-2003
LOCUS
DEFINITION
OGXAB64TH ZM.0.7_1.5_KB Zea mays genomic clone ZMMBMA0482K08,
genomic survey sequence.
ACCESSION
CC690447
VERSION
CC690447.1 GI:32095223
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 577)
Whiteclaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGXAB64TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR

FEATURES
source
Location/Qualifiers
1..577
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0482K08"
/clone_lib="ZM.0.7_1.5_KB"
/note="Vector: pBGSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 68.6%; Score 19.2; DB 29; Length 577;
Best Local Similarity 77.8%; Pred. No. 3.1e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CCATCTCTCANNATCCCTGCTGTG 28
|||||
Db 146 CCTGCTCGTCAGCATCCCTGCAGTTGG 172

RESULT 5
CD443887 646 bp mRNA linear EST 03-JUN-2003
LOCUS
DEFINITION
ELOIN0432D03.b Endosperm_4 Zea mays cDNA, mRNA sequence.
ACCESSION
CD443887
VERSION
CD443887.1 GI:31359530
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 646)
Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
Messing,J.
Sequencing of the maize endosperm ESTs
Unpublished (2002)
Contact: Lai, Jinheng
Dr. Joachim Messing's lab
Wakman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@wakman.rutgers.edu
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..846
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W22"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm_4"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 68.6%; Score 19.2; DB 14; Length 646;
Best Local Similarity 77.8%; Pred. No. 3.2e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCATCTCTCANNATCCCTGCTGTG 27
|||||
Db 276 CCGATGTCATCATTCCTCCGCTGTG 302

RESULT 6
AG063981/c 659 bp DNA linear GSS 03-NOV-2001
LOCUS
DEFINITION
Pan troglodytes DNA, clone: PTB-052019.F, genomic survey sequence.
ACCESSION
AG063981

```

```

VERSION AG063981.1 GI:16615783
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 659)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Aaso Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanzee@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
FEATURES
source Location/Qualifiers
1 .659
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-052019.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN
Query Match 68.6%; Score 19.2; DB 29; Length 659;
Best Local Similarity 77.8%; Pred. No. 3.2e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CCCATCTCNCANNATCCCTGCTGTTG 27
Db 626 CCCACCTCCACGATCCCGCTGTTG 600
RESULT 7
CG232800 938 bp DNA linear GSS 22-AUG-2003
LOCUS CG232800
DEFINITION CG2B120TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMWBma0752D15,
genomic survey sequence.
ACCESSION CG232800
VERSION CG232800.1 GI:34132686
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1
AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Reinick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nurnberg, A., Robbins, D. and Lakey, N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other GSSs: CG2B120TH
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843

```

```

Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
FEATURES
source Location/Qualifiers
1 .938
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMWBma0752D15"
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methylation filtered genomic DNA library"
ORIGIN
Query Match 68.6%; Score 19.2; DB 29; Length 938;
Best Local Similarity 77.8%; Pred. No. 3.7e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 CCATCTCNCANNATCCCTGCTGTTGG 28
Db 51 CCTGCTCGTCAGCATCCCTGCA GTTG 77
RESULT 8
CG456461/c 952 bp DNA linear GSS 17-SEP-2003
LOCUS PUIJW63TDB_ZM_0.6_1.0_KB_Zea_mays_genomic_clone_ZMWBta0600K05,
genomic survey sequence.
ACCESSION CG456461
VERSION CG456461.1 GI:34841461
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1
AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Reinick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other GSSs: PUIJW63TBB
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
FEATURES
source Location/Qualifiers
1 .952
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMWBta0600K05"
/clone_lib="ZM 0.6 1.0 KB"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
ORIGIN
Query Match 68.6%; Score 19.2; DB 29; Length 952;
Best Local Similarity 77.8%; Pred. No. 3.8e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 CCATCTCNCANNATCCCTGCTGTTGG 28
Db 895 CCTGCTCGTCAGCATCCCTGCA GTTG 869

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RESULT 11	
CC187707	1139 bp DNA linear GSS 08-MAY-2003
LOCUS	CH261-33N7.Sp6.1 CH261 Gallus gallus genomic clone CH261-33N7,
DEFINITION	genomic survey sequence.
ACCESSION	CC187707
VERSION	CC187707.1 GI:30431607
KEYWORDS	GSS.
SOURCE	Gallus gallus (chicken)
ORGANISM	Gallus gallus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
	Phasianinae; Gallus.
	1 (bases 1 to 1139)
REFERENCE	Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
AUTHORS	Warren, W., Graves, T., Mardis, E. and Wilson, R.
TITLE	Gallus gallus BAC End Reads
JOURNAL	Unpublished (2003)
COMMENT	Contact: Richard K. Wilson Genome Sequencing Center Washington University School of Medicine Email: submissions@watson.wustl.edu Insert Length: 18200 Std Error: 0.00 Seq primer: Sp6 ATTTAGGTGACACTATAG

Class: BAC ends
High quality sequence start: 145
High quality sequence stop: 618.

FEATURES

Location/Qualifiers
1..1139
/organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-33N7"
/sex="female"
/cell_line="UCD001, inbred 256"
/clone_lib="CH261"
/notes="Vector: pPARAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CH261 Female Chicken library - For library and clone
ordering information: <http://www.chori.org/bacpac>

ORIGIN

Query Match 68.6%; Score 19.2; DB 28; Length 1139;
Best Local Similarity 77.8%; Pred. No. 4e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCATCTCCTCANNATCCCTGCTGTGG 28

Db 131 CCAGCTCATCTATATCTCTGCTGTGG 157

RESULT 12

BC026893/c
LOCUS
DEFINITION
Mus musculus downstream of Skil1, mRNA (cdna clone IMAGE:3982045),
with apparent retained intron.

ACCESSION
BC026893

VERSION
BC026893.1 GI:22268016

KEYWORDS
HTC.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2314)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heideh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Udwin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Bladesley, R.W., Touchman, J.W., Green, E.D.,
Dackson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,
Schnerker, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

PUBMED
12477932

2 (bases 1 to 2314)

Strausberg, R.

Direct Submission

Submitted (04-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 40 Row: i Column: 24
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis

This clone has the following problem: retained intron.

FEATURES

Location/Qualifiers

1..2314

/organism="Mus musculus"

/mol_type="mRNA"

/strain="Czech II"

/db_xref="taxon:10090"

/clone="IMAGE:3982045"

/tissue_type="Mammary tumor metastasized to lung. Tumor

arose spontaneously from a senescent normal mammary

(clonal) outgrowth infected with the virus MMTV."

/clone_lib="NCI_CGAP_Lu29"

/lab_host="DH10B"

/notes="Vector: pCMV-SPORT6"

ORIGIN

Query Match 68.6%; Score 19.2; DB 11; Length 2314;
Best Local Similarity 77.8%; Pred. No. 5.4e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCANNATCCCTGCTGTGG 27

Db 1769 CCATCTGTCATCTCCTGCTGTGG 1743

RESULT 13

BF723268/c

LOCUS

DEFINITION

mab30a01.y1 Soares NMEBA branchial arch Mus musculus cDNA clone

IMAGE:3971616 5' similar to TR:Q93V6 Q93V6 HYPOTHETICAL 22.9 KD

PROTEIN ;, mRNA sequence.

ACCESSION

BF723268

VERSION

BF723268.1 GI:12024270

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 413)

REFERENCE

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Other ESTs: mab30a01.x1

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml

MGI:1471648

laser-captured isthmal cells from tox176 transgenic mice. 1st strand of cDNA was synthesized with reverse transcriptase and oligo(dT) beads, then cDNA was amplified by PCR using modified SMART primers. The final cDNA was cloned in pMP1 vector in annealing reaction with Uracil DNA Glycosylase (UDG). Library constructed by Y. Korshunova and M. Lovett. Library materials provided by Mills JC & Gordon JJ."

ORIGIN

Best Match 67.1%; Score 18.8; DB 14; Length 445;
Query Local Similarity 80.0%; Pred. No. 4e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCATCTTCNTCANNATCCCTGCTGT 25
||||| ||||| ||||| ||||| |||||
Db 224 CCAGATCATCAGGATCCCTGCTGT 200

RESULT 15
BI048424/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI048424 463 bp mRNA linear EST 14-JUN-2001
MR4-TN0112-080101-209-e05 TN0112 Homo sapiens cDNA, mRNA sequence.
BI048424
BI048424.1 GI:14455046
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 463)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-TN0112-
080101-209-e05&t3=2001-01-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 35
High quality sequence stop: 463.
Location/Qualifiers
1. .463
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="TN0112"
/note="Organ: Testis normal; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

FEATURES
source

Query Match 67.1%; Score 18.8; DB 12; Length 463;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCATCTCNCANNATCCCTGCTGTT 26
Db 43 CCATCCCATCACCAGCCCTGCTGTT 19

Search completed: August 3, 2004, 19:50:54
Job time : 1259 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 17:17:11 ; Search time 685.5 Seconds
(without alignments)
1770.394 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28
Sequence: 1 aaatcgtgaaacgcgagagaacccgcg 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	342	14	FLD2CPM2 X51709 Dengue-2 vi
2	28	100.0	840	14	AF360860 Dengue vi
3	28	100.0	840	14	AF360861 Dengue vi
4	28	100.0	840	14	AF360862 Dengue vi
5	28	100.0	840	14	AF360863 Dengue vi
6	28	100.0	2319	14	S66064 S66064 structural
7	28	100.0	2325	14	AF469175 Dengue vi
8	28	100.0	2325	14	AF469176 Dengue vi
9	28	100.0	2325	14	AF509530 Dengue vi
10	28	100.0	2325	14	AY044442 Dengue vi
11	28	100.0	2357	6	AR232496 AR232496 Sequence
12	28	100.0	2357	14	DEN2NGC D00346 Dengue viru
13	28	100.0	2469	14	DENJAMA M15075 Dengue viru
14	28	100.0	2552	14	AY152036 Dengue vi
15	28	100.0	2552	14	AY152040 Dengue vi
16	28	100.0	2552	14	AY152044 Dengue vi
17	28	100.0	2552	14	AY152048 Dengue vi
18	28	100.0	2552	14	AY152052 Dengue vi
19	28	100.0	2552	14	AY152056 Dengue vi
20	28	100.0	2552	14	AY152060 Dengue vi
21	28	100.0	2552	14	AY152064 Dengue vi
22	28	100.0	2552	14	AY152068 Dengue vi
23	28	100.0	2552	14	AY152072 Dengue vi
24	28	100.0	2552	14	AY152076 Dengue vi
25	28	100.0	2552	14	AY152080 Dengue vi
26	28	100.0	2552	14	AY152084 Dengue vi
27	28	100.0	2552	14	AY152088 Dengue vi
28	28	100.0	2552	14	AY152092 Dengue vi
29	28	100.0	2552	14	AY152096 Dengue vi
30	28	100.0	2552	14	AY152100 Dengue vi
31	28	100.0	2552	14	AY152104 Dengue vi
32	28	100.0	2552	14	AY152108 Dengue vi
33	28	100.0	2552	14	AY152112 Dengue vi
34	28	100.0	2552	14	AY152116 Dengue vi
35	28	100.0	2552	14	AY152120 Dengue vi
36	28	100.0	2552	14	AY152124 Dengue vi
37	28	100.0	2552	14	AY152128 Dengue vi
38	28	100.0	2552	14	AY152132 Dengue vi
39	28	100.0	2552	14	AY152136 Dengue vi
40	28	100.0	2552	14	AY152140 Dengue vi
41	28	100.0	2552	14	AY152144 Dengue vi
42	28	100.0	2552	14	AY152148 Dengue vi
43	28	100.0	2552	14	AY152152 Dengue vi
44	28	100.0	2552	14	AY152156 Dengue vi
45	28	100.0	2552	14	AY152160 Dengue vi

ALIGNMENTS

RESULT 1
FLD2CPM2 342 bp RNA linear VRL 10-FEB-1999
LOCUS Dengue-2 virus RNA for capsid protein, partial, from a case of
DEFINITION dengue shock syndrome (M2) .
ACCESSION X51709
VERSION X51709.1 GI:59299
KEYWORDS capsid protein.
SOURCE Dengue virus type 2
ORGANISM Dengue virus type 2
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
AUTHORS Flavivirus; Dengue virus group.
TITLE 1 (bases 1 to 342)
Samuel S., Koh, C.L., Pang, T. and Lam, S.K.
Nucleotide and encoded amino acid sequences of the capsid protein

gene of three dengue-2 viruses isolated in Malaysia from patients with dengue haemorrhagic fever, dengue shock syndrome or dengue fever

Nucleic Acids Res. 18 (7), 1904 (1990)

90245598

PUBLISHED

2 (bases 1 to 342)

REFERENCE

Koh,C.L.

AUTHORS

Direct Submission

JOURNAL

Submitted (05-FEB-1990) Koh C.-L., University of Malaysia,

Department of Genetics and Cellular Biology, 5910 Kuala Lumpur,

Malaysia

COMMENT

See <M15075> and <M19197> for previously reported sequence. See

<X51708> and <X51710> for capsid protein sequences of M1 and M3.

FEATURES

Location/Qualifiers

1..342

/organism="Dengue virus type 2"

/mol_type="genomic RNA"

/strain="M2, isolated from case of dengue shock syndrome"

/db_xref="taxon:11060"

1..342

/note="unnamed protein product; capsid protein, partial

(AA 1-114)"

/codon_start=1

/protein_id="CAA36005.1"

/db_xref="GI:59300"

/db_xref="GOA:O89715"

/db_xref="SPRMBL:O89715"

/translation="MNDQRKARSTPFNMLKRNVRVSTVQQLTKRFSGLMLOGRGLP

KLFMALVAFRLFTIPPTAGILKRWGTIKKSKAINVLRGFRKEIGRMNLINRRRTA

GVIIIMLIPTVMA"

ORIGIN

Query Match

Best Local Similarity

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY

1 AATATGCTGAACCGCGAGAGAACCGCG 28

|||||

40 AATATGCTGAACCGCGAGAGAACCGCG 67

Db

RESULT 2

AF360860

LOCUS

Dengue virus type 2 isolate LARD1432 polyprotein gene, partial cds.

AF360860

ACCESSION

AF360860.1 GI:18644121

VERSION

KEYWORDS

SOURCE

ORGANISM

Dengue virus type 2

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

REFERENCE

1 (bases 1 to 840)

Uzategui,N.Y., Camacho,D., Comach,G., Cuello de Uzategui,R.,

Holmes,E.C. and Gould,E.A.

AUTHORS

Molecular epidemiology of dengue type 2 virus in Venezuela:

evidence for in situ virus evolution and recombination

J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)

JOURNAL

MEDLINE

21571640

PUBLISHED

11714970

REFERENCE

2 (bases 1 to 840)

Uzategui,N.Y., Camacho,D., Comach,G., Cuello de Uzategui,R.,

Holmes,E.C. and Gould,E.A.

AUTHORS

Direct Submission

JOURNAL

Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,

Oxford OX2 6UD, England

Location/Qualifiers

1..840

/organism="Dengue virus type 2"

/mol_type="genomic RNA"

/isolate="LARD1432"

/db_xref="taxon:11060"

FEATURES

source

100.0%; Score 28; DB 14; Length 840;

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY

1 AATATGCTGAACCGCGAGAGAACCGCG 28

|||||

40 AATATGCTGAACCGCGAGAGAACCGCG 67

Db

RESULT 3

AF360861

LOCUS

Dengue virus type 2 isolate LARD1701 polyprotein gene, partial cds.

AF360861

ACCESSION

AF360861.1 GI:18644123

VERSION

KEYWORDS

SOURCE

ORGANISM

Dengue virus type 2

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

REFERENCE

1 (bases 1 to 840)

Uzategui,N.Y., Camacho,D., Comach,G., Cuello de Uzategui,R.,

Holmes,E.C. and Gould,E.A.

AUTHORS

Molecular epidemiology of dengue type 2 virus in Venezuela:

evidence for in situ virus evolution and recombination

J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)

JOURNAL

MEDLINE

21571640

PUBLISHED

11714970

REFERENCE

2 (bases 1 to 840)

Uzategui,N.Y., Camacho,D., Comach,G., Cuello de Uzategui,R.,

Holmes,E.C. and Gould,E.A.

AUTHORS

Direct Submission

JOURNAL

Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,

Oxford OX2 6UD, England

Location/Qualifiers

1..840

/organism="Dengue virus type 2"

/mol_type="genomic RNA"

/isolate="LARD1701"

/db_xref="taxon:11060"

FEATURES

source

100.0%; Score 28; DB 14; Length 840;

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY

1 AATATGCTGAACCGCGAGAGAACCGCG 28

|||||

40 AATATGCTGAACCGCGAGAGAACCGCG 67

Db

RESULT 3

AF360861

LOCUS

Dengue virus type 2 isolate LARD1701 polyprotein gene, partial cds.

AF360861

ACCESSION

AF360861.1 GI:18644123

VERSION

KEYWORDS

SOURCE

ORGANISM

Dengue virus type 2

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

REFERENCE

1 (bases 1 to 840)

Uzategui,N.Y., Camacho,D., Comach,G., Cuello de Uzategui,R.,

Holmes,E.C. and Gould,E.A.

AUTHORS

Molecular epidemiology of dengue type 2 virus in Venezuela:

evidence for in situ virus evolution and recombination

J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)

JOURNAL

MEDLINE

21571640

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REFERENCE

2 (bases 1 to 840)

Uzategui,N.Y., Camacho,D., Comach,G., Cuello de Uzategui,R.,

Holmes,E.C. and Gould,E.A.

AUTHORS

Direct Submission

JOURNAL

Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,

Oxford OX2 6UD, England

Location/Qualifiers

1..840

/organism="Dengue virus type 2"

/mol_type="genomic RNA"

/isolate="LARD1701"

/db_xref="taxon:11060"

FEATURES

source

100.0%; Score 28; DB 14; Length 840;

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY

1 AATATGCTGAACCGCGAGAGAACCGCG 28

|||||

40 AATATGCTGAACCGCGAGAGAACCGCG 67

Db

RESULT 3

AF360861

LOCUS

Dengue virus type 2 isolate LARD1701 polyprotein gene, partial cds.

AF360861

ACCESSION

AF360861.1 GI:18644123

VERSION

KEYWORDS

SOURCE

ORGANISM

Dengue virus type 2

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

REFERENCE

1 (bases 1 to 840)

Uzategui,N.Y., Camacho,D., Comach,G., Cuello de Uzategui,R.,

Holmes,E.C. and Gould,E.A.

AUTHORS

Molecular epidemiology of dengue type 2 virus in Venezuela:

evidence for in situ virus evolution and recombination

J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)

JOURNAL

MEDLINE

21571640

PUBLISHED

11714970

REFERENCE

2 (bases 1 to 840)

Uzategui,N.Y., Camacho,D., Comach,G., Cuello de Uzategui,R.,

Holmes,E.C. and Gould,E.A.

AUTHORS

Direct Submission

JOURNAL

Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,

Oxford OX2 6UD, England

Location/Qualifiers

1..840

/organism="Dengue virus type 2"

/mol_type="genomic RNA"

/isolate="LARD1701"

/db_xref="taxon:11060"

FEATURES

source

100.0%; Score 28; DB 14; Length 840;

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY

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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
    |||||
Db 40 AATATGCTGAACCGCGAGAGAAACCGCG 67

RESULT 4
AF360862 840 bp ss-RNA linear VRL 11-FEB-2002
LOCUS Dengue virus type 2 isolate LARD1910 polyprotein gene, partial cds.
DEFINITION AF360862
ACCESSION AF360862
VERSION AF360862.1 GI:18644125
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 840)
Uzcatogui,N.Y., Camacho,D., Comach,G., Cuello de Uzcatogui,R.,
Holmes,E.C. and Gould,E.A.
Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
21571640
PUBMED 11714970
REFERENCE
2 (bases 1 to 840)
Uzcatogui,N.Y., Camacho,D., Comach,G., Cuello de Uzcatogui,R.,
Holmes,E.C. and Gould,E.A.
Direct Submission
Submitted (15-MAR-2001)
Oxford OX2 6UD, England
Location/Qualifiers
source
1..840
/organism="Dengue virus type 2"
/mol_type="genomic RNA"
/isolate="LARD1910"
/db_xref="taxon:11060"
/country="Venezuela"
1..>840
/note="contains capsid, premembrane, and membrane
proteins"
/codon_start=1
/product="polyprotein"
/protein_id="AAL76290.1"
/db_xref="GI:18644126"
/translation="MNNQRKKARSTPFNMLKRNRVSTVQQLTKRFSGLMQLQGRGPL
KLFMALVAFRLFTIPPTAGILKRWGTIKKSKAINVLRGFRKEIGRMILNLRRTA
GVIIMLIPTAMAFHLTRNGEPHMYVGRQKSLFKFTEDGVNMTCTMAIDLGEICE
DTITYKCPLLRQNEPEDIDWCNISTSTWVTYGTCTTGBHREKRSVALVPHVGMGLE
TRTETWMSSEGAKWKVQRIETLWRHPGFAMAAILAYTIGTTFQKALIFILLTAVA
PSMT"

CDS
1..>840
/note="contains capsid, premembrane, and membrane
proteins"
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KLFMALVAFRLFTIPPTAGILKRWGTIKKSKAINVLRGFRKEIGRMILNLRRTA
GVIIMLIPTAMAFHLTRNGEPHMYVGRQKSLFKFTEDGVNMTCTMAIDLGEICE
DTITYKCPLLRQNEPEDIDWCNISTSTWVTYGTCTTGBHREKRSVALVPHVGMGLE
TRTETWMSSEGAKWKVQRIETLWRHPGFAMAAILAYTIGTTFQKALIFILLTAVA
PSMT"

ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 840;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
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Db 40 AATATGCTGAACCGCGAGAGAAACCGCG 67

RESULT 6
S66064 2319 bp DNA linear VRL 04-DEC-1993
LOCUS structural polyprotein [dengue type 4 virus DEN4, H241-P, Genomic,
DEFINITION 2319 nt].
ACCESSION S66064
VERSION S66064.1 GI:432575
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 4
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2319)
Kawano,H., Rostapshov,V., Rosen,L. and Lai,C.J.
Genetic determinants of dengue type 4 virus neurovirulence for mice
J. Virol. 67 (11), 6567-6575 (1993)
94016840
PUBMED 8411360
REMARK
Gensbank staff at the National Library of Medicine created this
entry [NCBI gisseq 138430] from the original journal article.
This sequence comes from Fig. 1.

FEATURES
Location/Qualifiers
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Flavivirus; Dengue virus group.
1 (bases 1 to 840)
Uzcatogui,N.Y., Camacho,D., Comach,G., Cuello de Uzcatogui,R.,
Holmes,E.C. and Gould,E.A.
Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
21571640
PUBMED 11714970
REFERENCE
2 (bases 1 to 840)
Uzcatogui,N.Y., Camacho,D., Comach,G., Cuello de Uzcatogui,R.,
Holmes,E.C. and Gould,E.A.
Direct Submission
Submitted (15-MAR-2001)
Oxford OX2 6UD, England
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QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
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Db 40 AATATGCTGAACCGCGAGAGAAACCGCG 67

RESULT 6
S66064 2319 bp DNA linear VRL 04-DEC-1993
LOCUS structural polyprotein [dengue type 4 virus DEN4, H241-P, Genomic,
DEFINITION 2319 nt].
ACCESSION S66064
VERSION S66064.1 GI:432575
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 4
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2319)
Kawano,H., Rostapshov,V., Rosen,L. and Lai,C.J.
Genetic determinants of dengue type 4 virus neurovirulence for mice
J. Virol. 67 (11), 6567-6575 (1993)
94016840
PUBMED 8411360
REMARK
Gensbank staff at the National Library of Medicine created this
entry [NCBI gisseq 138430] from the original journal article.
This sequence comes from Fig. 1.

FEATURES
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RESULT 7
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LOCUS
DEFINITION
Dengue virus type 2 strain GD24/93 polyprotein gene, partial cds.
ACCESSION
AF469175
VERSION
AF469175.1 GI:18766554
KEYWORDS
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2325)
AUTHORS
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
Zhao,W.Z.
TITLE
Structural genes of dengue virus type 2 strain GD24/93 isolate from
Nanhai, Guangdong, China
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 2325)
AUTHORS
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
Zhao,W.Z.
TITLE
Direct Submission
Submitted (16-JAN-2002) Department of Virology, The Military
Medical Institute of Guangzhou Military District, Dong Guanzhuang
Road 91, Guangzhou, Guangdong 5105407, China
FEATURES
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 40 AATATGCTGAACCGGAGAGAAACCGCG 67
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RESULT 8

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AF469176
LOCUS
DEFINITION
Dengue virus type 2 strain GD08/98 polyprotein gene, partial cds.
ACCESSION
AF469176
VERSION
AF469176.1 GI:18766556
KEYWORDS
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2325)
AUTHORS
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
Zhao,W.Z.
TITLE
Structural genes of dengue virus type 2 strain GD24/93 isolate from
Nanhai, Guangdong, China
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 2325)
AUTHORS
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
Zhao,W.Z.
TITLE
Direct Submission
Submitted (16-JAN-2002) Department of Virology, The Military
Medical Institute of Guangzhou Military District, Dong Guanzhuang
Road 91, Guangzhou, Guangdong 5105407, China
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QY 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
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Db 40 AATATGCTGAAACCGGAGAGAAACCGCG 67

RESULT 9
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DEFINITION
Dengue virus type 2 polyprotein gene, partial cds.
ACCESSION
AF509530
VERSION
AF509530.1 GI:21070436
KEYWORDS
Dengue virus type 2
SOURCE
Dengue virus type 2
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2325)
Ren,R., Yu,F., Dong,T., Wei,L., Hua,J., Yan,H. and Feng,C.
Isolation, identification and sequence analyses of dengue virus
type 2 strain GD19/2001
Unpublished
JOURNAL
2 (bases 1 to 2325)
Ren,R., Yu,F., Dong,T., Wei,L., Hua,J., Yan,H. and Feng,C.
Direct Submission
TITILE
Submitted (06-MAY-2002) Microbiology Department, The Military
Medical Institute of Guangzhou Military District, Dongguanhuang
Road, Guangzhou 510507, China
JOURNAL
FEATURES
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Db 40 AATATGCTGAAACCGGAGAGAAACCGCG 67

RESULT 10
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LOCUS
DEFINITION
Dengue virus type 2 strain Mara3 polyprotein gene, partial cds.
ACCESSION
AY044442
VERSION
AY044442.1 GI:18643733
KEYWORDS
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SOURCE
Dengue virus type 2
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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REFERENCE
1 (bases 1 to 2325)
Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
21571640
11714970
2 (bases 1 to 2325)
Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.M.,
Holmes,E.C. and Gould,E.A.
Direct Submission
TITILE
Submitted (09-JUL-2001) Flavivirus Group, CEH-Oxford, Mansfield
Road, Oxford OX1 3SR, United Kingdom
JOURNAL
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ORIGIN
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RESULT 9
AF509530
LOCUS
DEFINITION
Dengue virus type 2 polyprotein gene, partial cds.
ACCESSION
AF509530
VERSION
AF509530.1 GI:21070436
KEYWORDS
Dengue virus type 2
SOURCE
Dengue virus type 2
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2325)
Ren,R., Yu,F., Dong,T., Wei,L., Hua,J., Yan,H. and Feng,C.
Isolation, identification and sequence analyses of dengue virus
type 2 strain GD19/2001
Unpublished
JOURNAL
2 (bases 1 to 2325)
Ren,R., Yu,F., Dong,T., Wei,L., Hua,J., Yan,H. and Feng,C.
Direct Submission
TITILE
Submitted (06-MAY-2002) Microbiology Department, The Military
Medical Institute of Guangzhou Military District, Dongguanhuang
Road, Guangzhou 510507, China
JOURNAL
FEATURES
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Query Match      100.0%; Score 28; DB 14; Length 2325;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
    |||||
Db 40 AATATGCTGAAACCGGAGAGAAACCGCG 67

RESULT 10
AY044442
LOCUS
DEFINITION
Dengue virus type 2 strain Mara3 polyprotein gene, partial cds.
ACCESSION
AY044442
VERSION
AY044442.1 GI:18643733
KEYWORDS
Dengue virus type 2
SOURCE
Dengue virus type 2
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2325)
Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
21571640
11714970
2 (bases 1 to 2325)
Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.M.,
Holmes,E.C. and Gould,E.A.
Direct Submission
TITILE
Submitted (09-JUL-2001) Flavivirus Group, CEH-Oxford, Mansfield
Road, Oxford OX1 3SR, United Kingdom
JOURNAL
FEATURES
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Location/Qualifiers
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DTITVNCPLLRQNEPEDIDWCNSTSTWVTYGTCTTGTGHRREKRSVALVPHVGMGLE
TRTETWMSSEGAKHQAQRIETVLRHPGFTINAVILAYTIGTYFORVILFILLTAVA
PSMTMRCIGISNRDFFGVSGGSWVDIVLEHGSCTVTMAKNRPTLDLFDLTKTEAKHPA
TURKCIKALNTTITASRCPTQGEPSLNEEQDKRFCKHSMVDRGNGCGLFGKGG
IVTCAMFTCKNMGKVVLPENLEYITVITPHSGEHAAGVNDTGKHGEIKITPOSSI
TEAELTGYGTVMTEGSPRTGLDFNEMVLQMEKAWLVHROFLDLPLPWLPGAEATQG
SNWIOKETLVTFKNPHAKQDVVVLGSOEGAMHTALTGATEIQMSSGNLFTGHLKCR
LRMDLQKMGYSNCTCKEIKVIEATQHGTVIRVQYEGGSPCKIPFIMDLKX
RHLVGLRLITVNPVTEKDSPVNIEAPFPFGDSYIIIGVPEGQKLKSWFKGSGSIQGMF
ETTMGAKMMAILGTAWDFGSLGGVFTSIGKALHQVFGAIYGAAPSGVSWTMKILIG
VIITWGMNRSSTLSVSLVGVITVLYLGMVQA"

CDS
mat_peptide
/product="capsid protein"
/notes="C"
451. .840
/product="premembrane/membrane protein"
/notes="p1m (M)"
841. .2325
/product="envelope protein"
/notes="E; structural protein"

ORIGIN
Query Match      100.0%; Score 28; DB 14; Length 2325;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
    |||||
Db 40 AATATGCTGAAACCGGAGAGAAACCGCG 67

RESULT 11
AR232496
```

LOCUS	AR232496	2357 bp	RNA	linear	PAT 20-DEC-2002							
DEFINITION	Sequence 1 from patent US 6455509.											
ACCESSION	AR232496											
VERSION	AR232496.1	GI:27274633										
KEYWORDS												
SOURCE	Unknown.											
ORGANISM	Unknown.											
REFERENCE	Unclassified.											
AUTHORS	Kocheil,T.J., Porter,K.R., Raviprakash,K., Hoffman,S.L. and Hayes,C.G.											
TITLE	Dengue nucleic acid vaccines that induce neutralizing antibodies											
JOURNAL	Patent: US 6455509-A 1 24-SEP-2002;											
FEATURES	Location/Qualifiers											
source	1. .2357											
	/organism="unknown"											
	/mol_type="genomic RNA"											
ORIGIN												
Query Match	100.0%; Score 28; DB 6; Length 2357;											
Best Local Similarity	100.0%; Pred. No. 0.13;											
Matches	28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
QY	1 AATATGCTGAACGCGAGAGAAACCGCG 28											
Db	60 AATATGCTGAACGCGAGAGAAACCGCG 87											
RESULT 12												
DEN2NGC												
LOCUS	Dengue virus type 2 gene for polyprotein, partial cds, strain:New Guinea C.											
DEFINITION	Dengue virus type 2 gene for polyprotein, partial cds, strain:New Guinea C.											
ACCESSION	D00346											
VERSION	D00346.1	GI:221230										
KEYWORDS												
SOURCE	Dengue virus type 2											
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.											
REFERENCE	1 (bases 1 to 2357)											
AUTHORS	Gruenberg,A., Woo,W.S., Biedrzycka,A. and Wright,P.J.											
TITLE	Partial nucleotide sequence and deduced amino acid sequence of the structural proteins of dengue virus type 2, New Guinea C and PUO-218 strains											
JOURNAL	J. Gen. Virol.	69 (Pt 6),	1391-1398	(1988)								
MEDLINE	88258474											
PUBMED	3385407											
COMMENT	Nucleotide 1 in the NGC sequence corresponds to nucleotide 77 from the 5'end of the DEN-2(JAM) sequence.											
FEATURES	Location/Qualifiers											
source	1. .2357											
	/organism="Dengue virus type 2"											
	/mol_type="genomic RNA"											
	/strain="New Guinea. C"											
	/db_xref="taxon:11060"											
	/note="20bp upstream from the C protein amino terminal end"											
CDS	21. .>2357											
	/codon_start=1											
	/product="polyprotein"											
	/protein_id="BA00255.1"											
	/db_xref="GI-221231"											
	/translation="MNNQRKARNTPNMLKRENRVSTVQQLTKRPSLGMQGRGLPKLMAVFAVRFLRTITPTAGILIKRWGITKSKAINVLVRFRKIGRLMNLINRRRTAKLMIMLIPYVTHFLTRNPEHMIIVSRQKGSLLFKPTGDVNMCTLMAMDIGLGELEDTTYKCPFRQNEPQIDWCNCTSTWVTGCTTGEHRREKRSVALVPHVGMGLETRTETWMSKQKWAQRIETWILRHFGFTIMAILAYTGTTHFORALIIFLLTAVAPSNMTKCIIGISNDRDFVEGVSQGSNDVILEHGSCTVMAKNKPFILPELLKTEAKQAPALTKRYCIAELKNTTIDUSRCPTGSELSNEQKRFVCKHSDVRGMNGCGGLFGKGGIVTCAMPTCKNNKMKVYQENLEYITIVIPHSGEHAVGNDTGKHGKEIKITPQSIITAEALGTGVTYMECSPTKQDNEVMVLLQNMENKAWLVRQWFLDLPLPWLPGADGTQSNWIOKLEITFKNKGAKQDVVVLGSOEGAMHITALTGATEIOWSSGNLLFTGHLKCRPL											

mat_peptide /product="membrane protein"
937. .2421
mat_peptide /product="envelope protein"
2422. .>2469
mat_peptide /product="nonstructural protein"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2469;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCAGAGAAACCGCG 28
|||||
DB 136 AATATGCTGAACCGCAGAGAAACCGCG 163
|||||

RESULT 14

AY152036S1 2552 bp RNA linear VRL 29-SEP-2003
LOCUS
DEFINITION
Dengue virus type 4 D4.20_1998 polyprotein precursor, gene, partial cds.

ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE

AY152036
AY152036.1 GI:28170806

1 of 4

Dengue virus type 4 (DEN-4)

Dengue virus type 4

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

1 (bases 1 to 2552)

Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,

Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.

Selection-Driven Evolution of Emergent Dengue Virus

Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

12832629

2 (bases 1 to 2552)

Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,

Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.

Direct Submission

Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio

Piedras, PO Box 23360, San Juan 00931, Puerto Rico

FEATURES

source

1. .>2552

/organism="Dengue virus type 4"

/mol_type="genomic RNA"

/isolate="D4.20 1998"

/db_xref="taxon:11070"

/country="Puerto Rico"

/notes="acronym: DEN-4"

CDS

1. .>2552
/notes="contains core protein, matrix protein and envelope glycoprotein"
/codon_start=1
/product="polyprotein precursor"
/protein_id="AAN3823.1"
/db_xref="GI:28170813"

/translation="MNQRKKVVRPPFNMLKRERNRVSTPQGLVKRFSTGLFSGKGLPLR
MYLAFITFLRVLSIPTAGILRWGQKKNKAIKILIGRKEIGRMNLINLGRKRSTI
TLLCLIPVTAMPHLSTRDGEPLMI VAKHERGRPLLPKTTGKCTLIAMDIGEMCED
TVTYKCLPLVNTPEPIDDCNCLTSTWWMYGTCTOSGERRERKRSVALTPHSGMGLT
RAETWMSSEGAKHAQRVESWILRNPFGALLAGMAYMIGQTGIQRTVFVLMVLVAP
SYGMRGVGNRDRFVGVSGGAWDLVLEHGGCVTTMAQKPTLDPELTKTTFKTAKEVAL
LRTYCEASISNITTATRCPTGEPYKEEQDQYICRRDVVDVDRGNGCGLFGKGGV
VTCAKFSCSGKITGNLVQENLEYVTVVTHNGDTHAVGNDTSNHGVATITPRSPSV
EVKLDPYGBELTLDCEPRSGIDENEMILMKMKKTWLHVQKWFLLDPLPWTAGDTSEV
HNKLRKIMSYTMCNKGKSIDKEMAEQHTQTVTVKYGEGAGACPKPIERDVNKE
RVKVRVISTPLAENTNVTNIELEPPFGDSITIVGVNSALTJLHFWKSGSIRIGKFE
STYRKAKRMALIGETAWDFVSGVGLFTSLGKAVHQVFGSVYTMFGVSWMIRILIGF
LVLMIGTNSRNTSMAMTCIAGGGITLFLGFTVQADMGCVWSWSGRELKCGSIGFVGDN
VHTWTEQYKIQPESPARLASAILNAHKDGVCGVIGIRSTTRLENVWMKQITNELN"

ORIGIN

QY 1 AATATGCTGAACCGCAGAGAAACCGCG 28
|||||
DB 136 AATATGCTGAACCGCAGAGAAACCGCG 163
|||||

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCAGAGAAACCGCG 28
|||||
DB 37 AATATGCTGAACCGCAGAGAAACCGCG 64
|||||

RESULT 15

AY152040S1
LOCUS
DEFINITION

AY152040

AY152040.1 GI:28170815

1 of 4

Dengue virus type 4 (DEN-4)

Dengue virus type 4

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

1 (bases 1 to 2552)

Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,

Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.

Selection-Driven Evolution of Emergent Dengue Virus

Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

12832629

2 (bases 1 to 2552)

Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,

Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.

Direct Submission

Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio

Piedras, PO Box 23360, San Juan 00931, Puerto Rico

FEATURES

source

1. .>2552

/organism="Dengue virus type 4"

/mol_type="genomic RNA"

/isolate="D4.19 1998"

/db_xref="taxon:11070"

/country="Puerto Rico"

/notes="acronym: DEN-4"

CDS

1. .>2552
/notes="contains core protein, matrix protein and envelope glycoprotein"
/codon_start=1
/product="polyprotein precursor"
/protein_id="AAN3827.1"
/db_xref="GI:28170822"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCAGAGAAACCGCG 28
|||||
DB 37 AATATGCTGAACCGCAGAGAAACCGCG 64
|||||

Search completed: August 3, 2004, 19:08:57
Job time : 686.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 15:36:33 ; Search time 152.5 Seconds
(without alignments)
779.997 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28
Sequence: 1 aatatgctgaacgcgagagaaacccgcg 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124039041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	28	100.0	28	7 ABX15698	Abx15698 Dengue vi
2	28	100.0	2357	7 ABX13740	Abx13740 Dengue vi
3	28	100.0	3381	2 AAT47666	Aat47666 Dengue vi
4	28	100.0	3381	2 AAX25114	Aax25114 Dengue vi
5	28	100.0	10616	7 AAD53912	Aad53912 Dengue vi
6	28	100.0	10648	7 AAD14612	Aad14612 Wild-type
7	28	100.0	10648	7 AAD14613	Aad14613 Attenuate
8	28	100.0	10649	7 AAD53911	Aad53911 Recombina
9	28	100.0	10649	7 AAD53910	Aad53910 Dengue vi
10	28	100.0	10717	4 AAD14605	Aad14605 Dengue vi
11	28	100.0	10723	2 AAQ12787	Aaq12787 Dengue 2
12	28	100.0	10723	2 AAT49303	Aat49303 cDNA sequ
13	28	100.0	10723	2 AAT49304	Aat49304 cDNA enco
14	28	100.0	10723	4 AAD14614	Aad14614 Dengue vi
15	28	100.0	10723	4 AAD14607	Aad14607 Wild-type
16	28	100.0	10723	4 AAD14606	Aad14606 Dengue vi
17	28	100.0	10723	4 AAD14608	Aad14608 Attenuate
18	28	100.0	10756	4 AAD14609	Aad14609 Dengue vi
19	26.4	94.3	10718	2 AAQ51476	Aaq51476 DEN1-S275
20	26.4	94.3	10723	4 AAD14603	Aad14603 Dengue vi
21	26.4	94.3	10723	4 AAD14604	Aad14604 Dengue vi
22	26.4	94.3	10735	4 AAD14602	Aad14602 Attenuate
23	26.4	94.3	10735	4 AAD14601	Aad14601 Wild-type

24	26	92.9	26	3 AAC68744	Aac68744 Dengue vi
25	26	92.9	28	2 AAT75917	Aat75917 DEN-2 clo
26	24.8	88.6	10699	4 AAD14610	Aad14610 Wild-type
27	24.8	88.6	10699	4 AAD14611	Aad14611 Attenuate
28	22	78.6	72	6 AAF88836	Aaf88836 Green flu
c 29	19.2	68.6	1083	3 AAC44997	Aac44997 Arabidops
c 30	19	67.9	765	6 ABQ34003	Abq34003 Oligonuel
c 31	19	67.9	765	6 ABQ34002	Abq34002 Oligonuel
c 32	19	67.9	28564	9 ADD46068	Add46068 Human gen
c 33	18.8	67.1	1008	3 AAC46148	Aac46148 Arabidops
c 34	18.6	66.4	3002	4 ABL29849	AbL29849 Drosophil
c 35	18.6	66.4	7264	4 ABL29848	AbL29848 Drosophil
c 36	18.4	65.7	449	3 AAA82355	Aaa82355 N. mening
c 37	18.4	65.7	1443	3 AAZ36361	Aaz36361 DNA encod
c 38	18.4	65.7	1443	8 ABX16417	Abx16417 DNA encod
c 39	18.4	65.7	4512	2 AAQ22767	Aaq22767 JEV Nakay
c 40	18.4	65.7	10976	3 ABL50890	AbL50890 Japanese
c 41	18.4	65.7	12980	2 AAV59364	Aav59364 Hepatitis
c 42	18.4	65.7	12980	6 ABK87286	Abk87286 Hepatitis
c 43	18.4	65.7	12980	7 ACA62469	AcA62469 DNA encod
c 44	18.4	65.7	15065	3 AAZ36195	Aaz36195 Nucleotid
c 45	18.2	65.0	333	4 AAI81993	Aai81993 Human pol

ALIGNMENTS

RESULT 1
ABX15698
ID ABX15698 standard; DNA; 28 BP.
XX
AC ABX15698;
XX
DT 31-MAR-2003 (first entry)
XX
DE Dengue virus detection PCR primer #2.
XX
KW PCR; primer; ss; reverse transcriptase; RT-PCR; dengue fever; DF;
KW dengue haemorrhagic fever; virus; viral detection.
XX
OS Dengue virus.
XX
PN US2002155435-A1.
XX
PD 24-OCT-2002.
XX
PF 28-FEB-2002; 2002US-00085944.
XX
PR 01-MAR-2001; 2001US-0272535P.
XX
(WANG/) WANG W.
XX
Wang W;
XX
DR WPI; 2003-182625/18.
XX
PT New dengue virus-specific primers, useful for reverse transcriptase-
PT polymerase chain reaction assays, particularly for detecting or
PT quantitating dengue virus in a sample.
XX
PS Claim 28; Page 1; 6pp; English.
XX
CC This invention relates to novel Dengue virus reverse transcriptase (RT)
CC PCR primers which may be used to detect Dengue virus in a sample. Dengue
CC virus is a member of the flavivirus family and causes diseases including
CC dengue fever (DF) and dengue haemorrhagic fever. The invention also
CC comprises a method for detecting and quantitating dengue virus. The
CC dengue virus-specific primers of the invention are useful in reverse
CC transcriptase-polymerase chain reaction assays, particularly for
CC detecting or quantitating dengue virus in a sample. The present sequence
CC represents a dengue virus specific RT-PCR primer used in the method of
CC the invention

SQ Sequence 28 BP; 11 A; 6 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 7; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.0052;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGAGAGAAACCGCG 28
 |||||
 DB 1 AATATGCTGAACCGAGAGAAACCGCG 28

RESULT 2
 ABX13740
 ID ABX13740 standard; DNA; 2357 BP.
 XX
 AC ABX13740;
 XX
 DT 28-FEB-2003 (first entry)
 XX
 DE Dengue virus type 2 structural gene genome segment.

XX Pharmaceutical; ds; immune response; immunogenic; envelope; membrane;
 KW PreM; dengue virus; Den; serotype; flavivirus; Flaviviridae; antigen;
 KW mosquito; Aedes aegyptii; acute undifferentiated fever;
 KW dengue haemorrhagic fever; DHF; dengue shock syndrome; DSS;
 KW immune enhancement phenomenon; DNA vaccine; gene therapy; vaccine;
 KW structural gene; virucide.

XX Dengue virus.

OS US6455509-B1.

PN 24-SEP-2002.

XX 04-JUN-1997; 97US-00869423.

XX 04-JUN-1996; 96US-0017839P.

XX (USNA) US SEC OF NAVY.

XX Kocheil TV, Porter KR, Raviprakash K, Hoffman SL, Hayes CG;

XX WPI; 2003-066244/06.

XX New pharmaceutical compositions containing dengue nucleic acids, useful
 PT as a vaccine, particularly for inducing a protective immune response in
 PT mammalian subjects against the dengue virus infection.

XX Disclosure; Col 17-20; 26pp; English.

XX The invention discloses a pharmaceutical composition capable of inducing
 CC an immune response in a mammalian subject, comprising an immunogenic
 CC amount of a eukaryotic plasmid expression vector in pharmaceutical form,
 CC which includes the envelope and membrane (preM) genes of a dengue type 1,
 CC 2, 3, or 4 virus. Dengue virus (Den) belongs to the flavivirus genus of
 CC the family Flaviviridae and is a positive strand RNA virus encoding ten
 CC proteins. These genes are translated as a polypeptide which is cleaved by
 CC host and viral proteinases. The virus envelope protein is a major antigen
 CC which can be targeted by neutralising antibodies. The membrane protein
 CC also appears on the virion surface and is required for proper processing
 CC of the envelope protein. Dengue viruses are transmitted primarily by the
 CC mosquito, Aedes aegyptii, and can lead to human illnesses ranging from
 CC acute undifferentiated fever to dengue haemorrhagic fever (DHF) and
 CC dengue shock syndrome (DSS). Secondary infections, with a different
 CC serotype, may lead to an immune enhancement phenomenon. The compositions
 CC of the invention are DNA vaccines which are injected into the animal as a
 CC technique of gene therapy. The composition is useful as a vaccine,
 CC particularly for inducing a protective immune response in mammalian
 CC subjects against the dengue virus infection. The sequence presented is
 CC the dengue virus type 2 (Den 2) structural gene genome segment

XX Sequence 2357 BP; 782 A; 471 C; 595 G; 509 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 7; Length 2357;
 Best Local Similarity 100.0%; Pred. No. 0.009; 0; Indels 0; Gaps 0;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGAGAGAAACCGCG 28
 |||||
 DB 60 AATATGCTGAACCGAGAGAAACCGCG 87

RESULT 3

AAT47666

ID AAT47666 standard; cDNA; 3381 BP.

XX AC AAT47666;

XX 17-OCT-2003 (revised)

DT 19-MAY-1997 (first entry)

XX Dengue virus serotype 2 PR159/S1 mutant sequence.

XX DEN-2; flavivirus; envelope protein; immunisation; vaccine; ss.

XX Dengue virus; serotype 2.

XX Key Location/Qualifiers

FT mutation

FT /tag= a

FT /note= "codon GAG (Glu) at position 1216-1218 of PR159/S1

FT is GAA (Glu) in wild-type PR159"

FT /tag= b

FT /note= "codon GTT (Val) at position 1258-1260 of PR159/S1

FT is GTG (Val) in wild-type PR159"

FT /tag= c

FT /note= "codon GTT (Val) at position 1762-1764 of PR159/S1

FT is ATT (Ile) in wild-type PR159"

FT /tag= d

FT /note= "codon AGC (Ser) at position 1927-1929 of PR159/S1

FT is AGT (Ser) in wild-type PR159"

XX WO9637221-A1.

XX 28-NOV-1996.

XX 24-MAY-1996; 96WO-US007627.

XX 24-MAY-1995; 95US-00448734.

XX 07-JUN-1995; 95US-00488807.

XX 10-JUL-1995; 95US-00500469.

XX (HAWAII) HAWAII BIOTECHNOLOGY GROUP INC.

XX Ivy JM, Nakano E, Clements D;

XX WPI; 1997-020938/02.

XX P-PSDB; AAW09409.

XX Sub:unit vaccine against flavivirus infection - contg. recombinant

PT envelope protein in secretable form, used for immunising against

PT flavivirus infection.

XX Example 1; Fig 3A-D; 121pp; English.

XX A cDNA sequence of dengue virus serotype 2 (DEN-2) mutant strain PR159/S1
 CC shows 4 differences from the wild-type DEN-2 PR159. This results in a
 CC conservation mutation in domain B of S1 that may be involved in the
 CC attenuation of this small-plaque, temp.-sensitive variant. The cDNA
 CC encodes the capsid, pre-membrane, envelope and NS1 proteins (AAW09409) of
 CC the virus. The clone can be used to express recombinant secreted
 CC polypeptides, comprising portions of the envelope protein (esp. domain B,
 CC Gly296-Gly385), in eukaryotic hosts, e.g. yeast (see also AAT47667 and

```
CC AAT47703-04) and Drosophila, for use in subunit vaccines against viral
CC infection. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
    Query Match          100.0%; Score 28; DB 2; Length 3381;
    Best Local Similarity 100.0%; Pred. No. 0.0094;
    Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
   |||||
Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67

RESULT 4
AAX25114
ID AAX25114 standard; cDNA; 3381 BP.
XX
AC AAX25114;
XX
DT 17-OCT-2003 (revised)
DT 05-JUL-1999 (first entry)
XX
DE Dengue virus serotype 2 PR159/S1 viral capsid, prM, E, NS1 cDNA.
XX
KW Flavivirus; envelope protein; vaccine; infection; diagnosis; ss.
XX
OS Dengue virus; serotype 2.
XX
PN WO9906068-A2.
XX
PD 11-FEB-1999.
XX
PF 27-JUL-1998; 98WO-US015447.
XX
PR 31-JUL-1997; 97US-00904227.
XX
PA (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
XX
PI Ivy JM, Peters ID, Collier BG, McDonnell M, Harada KE;
XX
WPI; 1999-153454/13.
DR P-PSDB; AAY05522.
XX
PT Recombinant dimeric flaviviral envelope vaccine - comprising a dimeric
PT 80%E protein, useful for protecting against flavivirus, especially dengue
PT virus infections.
XX
PS Example 1; Fig 3A-D; 60pp; English.
XX
CC This cDNA sequence encodes the capsid, prM, envelope (E) and NS1 proteins
CC (see AAY05522) of serotype 2 dengue virus DEN-2 strain PR159/S1. This
CC strain served as the source for DEN-2 genes used in the invention. A
CC vaccine for protecting against flavivirus infection comprises a dimeric
CC 80% E protein that has been secreted as a recombinant protein from a
CC eukaryotic cell. 80% E indicates a C-terminally truncated flavivirus E.
CC The dimeric truncated E is formed: (1) by directly linking 2 tandem
CC copies of 80% E via a flexible tether; (2) via the formation of a leucine
CC zipper domain through the homodimeric association of 2 leucine zipper
CC helices each fused to the C-terminus of an 80% E molecule; or (3) via the
CC formation of a non-covalently associated four-helix bundle domain formed
CC upon association of two helix-turn-helix moieties attached to the C-
CC terminus of an 80% E molecule. Dimeric truncated DEN-2 E proteins are
CC efficiently secreted by recombinant cells, are easier to purify than
CC intracellular proteins, and generate a high titer neutralising antibody
CC response. The method is generally applicable to flaviviruses, in
CC particular dengue viruses such as DEN-2, where 80% E comprises amino
CC acids 1-395 of DEN-2 E. The products can also be used for diagnosis of
CC infection. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
    Query Match          100.0%; Score 28; DB 2; Length 3381;
    Best Local Similarity 100.0%; Pred. No. 0.0094;
    Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
   |||||
Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67

RESULT 5
AAX53912
ID AAX53912 standard; DNA; 10616 BP.
XX
AC AAX53912;
XX
DT 28-MAY-2003 (first entry)
XX
DE Dengue virus type 2 strain rDEN2/4delta30 DNA.
XX
KW Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX
OS Dengue virus.
XX
FH Key
FH CDS          Location/Qualifiers
FT          97..10263
FT          /*tag= a
FT          /product= "DEN4 strain rDEN2/4delta30 protein"
FT          97..438
FT          /*tag= c
FT          /product= "Anchored capsid protein"
FT          97..396
FT          /*tag= b
FT          /product= "Virion capsid protein"
FT          439..936
FT          /*tag= d
FT          /product= "Membrane precursor protein"
FT          712..936
FT          /*tag= e
FT          /product= "Membrane protein"
FT          937..2421
FT          /*tag= f
FT          /product= "Envelope protein"
FT          2422..3477
FT          /*tag= g
FT          /product= "NS1 protein"
FT          3478..4131
FT          /*tag= h
FT          /product= "NS2A protein"
FT          4132..4521
FT          /*tag= i
FT          /product= "NS2B protein"
FT          4522..6375
FT          /*tag= j
FT          /product= "NS3 protein"
FT          6376..6756
FT          /*tag= k
FT          /product= "NS4A protein"
FT          6757..6825
FT          /*tag= l
FT          /product= "NS4B protein"
FT          6826..7560
FT          /*tag= m
FT          /product= "NS5 protein"
FT          7561..10260
FT          /*tag= n
FT          /product= "NS5 protein"
XX
PN WO200295075-A1.
XX
PD 28-NOV-2002.
XX
PF 22-MAY-2002; 2002WO-US016308.
XX
PR 22-MAY-2001; 2001US-0293049P.
```

```

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (BLAN/) BLANEY J E.
XX
XX Whitehead SS, Murphy BR, Hanley KA;
XX
XX WPI; 2003-120809/11.
DR P-PSDB; AAE35314.
XX
XX New mutated flavivirus, useful for fine tuning the attenuation and growth
PT characteristics of dengue virus vaccines for the prevention and/or
PT treatment of dengue virus infection.
XX
XX Disclosure; Page 135-138; 246pp; English.
XX
XX The present invention relates to novel mutated flaviviruses comprising a
CC phenotype in which the viral genome is modified by introduction of a
CC mutation, singly or in combination, taken from mutations from recombinant
CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
CC mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
CC dengue type 4 virus. The methods and compositions of the invention are
CC useful for fine tuning the attenuation and growth characteristics of
CC dengue virus vaccines for the prevention and/or treatment of dengue virus
CC infection. The present sequence is Dengue virus type 4 strain
CC rDEN2/4delta30 DNA
XX
XX Sequence 10616 BP; 3365 A; 2219 C; 2743 G; 2289 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 28; DB 7; Length 10616;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db ||||||||||||||||||||||||||||
136 AATATGCTGAAACGCGAGAGAAACCGCG 163

RESULT 6
AAD14612
ID AAD14612 standard; cDNA; 10648 BP.
XX
AC AAD14612;
XX
XX 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
XX Wild-type, virulent DEN-4 1036 cDNA.
XX
XX Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal;
XX avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX
XX Dengue virus; type IV.
XX
XX Key Location/Qualifiers
FH 102..10265
FT /*tag= a
FT /*product= "DEN-4 1036 protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Buttrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
DR P-PSDB; AAE07991.
XX

```

```

PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
XX Example 3; Page 373-389; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes wild-type, virulent dengue-4 (DEN-4) 1036 virus protein
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, premembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 10648 BP; 3294 A; 2213 C; 2810 G; 2331 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 28; DB 4; Length 10648;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db ||||||||||||||||||||||||||||
138 AATATGCTGAAACGCGAGAGAAACCGCG 165

RESULT 7
AAD14613
ID AAD14613 standard; cDNA; 10648 BP.
XX
AC AAD14613;
XX
XX 01-NOV-2001 (first entry)
DT
XX
XX Attenuated, vaccine-strain DEN-4 PDK-48 variant cDNA.
XX
XX Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal; mutein;
XX avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
XX ss.
XX
XX Dengue virus; type IV.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH 102..10265
FT /*tag= a
FT /*product= "DEN-4 PDK-48 protein variant"
XX
XX mutation replace(1211, T)
FT mutation /*tag= b
FT mutation replace(1971, G)
FT mutation /*tag= c
FT mutation replace(3182, G)
FT mutation /*tag= d
FT mutation replace(6660, C)
FT mutation /*tag= e
FT mutation replace(6957, A)
FT mutation /*tag= f
FT mutation replace(7162, T)
FT mutation /*tag= g
FT mutation replace(7546, C)
FT mutation /*tag= h
FT mutation replace(7623, G)

```

```

FT XX /*tag= i
PN WO200160847-A2.
PD 23-AUG-2001.
XX
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CVH, Butrapet S, Gubler DL, Bhamarapavati N;
XX
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07992.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX PT vaccinating against a range of dengue viruses.
XX
XX Example 4; Page 397-413; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX CC comprising amino acid mutations in the non-structural proteins of a
XX CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX CC structural genes of the virus are used as a backbone into which the
XX CC structural protein genes of a second flavivirus strain are inserted.
XX CC These chimeric viruses elicit pronounced immunogenicity but lack the
XX CC accompanying clinical symptoms of viral disease. Attenuated chimeric
XX CC flaviviruses are combined in a pharmaceutical composition to confer
XX CC simultaneous immunity against several strains of pathogenic flaviviruses
XX CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX CC flavivirus chimeras are also used as immunogens or multivalent vaccines
XX CC to confer simultaneous protection against infections. The present cDNA
XX CC sequence encodes attenuated dengue-4 (DEN-4) PDK-48 virus protein variant
XX CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX CC contains 5' non-coding region followed by a capsid protein (C) encoding
XX CC region, premembrane/membrane protein (prM) encoding region, an envelope
XX CC protein (E) encoding region, followed by the region encoding non-
XX CC structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
XX CC non-coding region. DEN-4 virus passaged in primary dog kidney (PDK) cells
XX CC 48 times is designated as DEN-4 PDK-48 virus
XX
XX Sequence 10648 BP; 3294 A; 2214 C; 2807 G; 2333 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 28; DB 4; Length 10648;
XX Best Local Similarity 100.0%; Pred. NO. 0.011;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
XX Db 138 AATATGCTGAACGCGAGAGAAACCGCG 165
XX
XX RESULT 8
XX AAD53911
XX ID AAD53911 standard; DNA; 10649 BP.
XX
XX AC AAD53911;
XX
XX DT 28-MAY-2003 (first entry)
XX
XX DE Recombinant dengue virus type 4 strain rDEN4 DNA.
XX
XX KW Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX
XX OS Dengue virus.
XX
XX FH Key Location/Qualifiers
XX FT 102..10649
XX FT /*tag= a
XX FT /product= "DEN4 strain rDEN4 protein"

```

```

FT mat_peptide 102..440
FT /*tag= c
FT /product= "Anchored capsid protein"
FT mat_peptide 102..398
FT /*tag= b
FT /product= "Virion capsid protein"
FT mat_peptide 441..938
FT /*tag= d
FT /product= "Membrane precursor protein"
FT mat_peptide 714..938
FT /*tag= e
FT /product= "Membrane protein"
FT mat_peptide 939..2423
FT /*tag= f
FT /product= "Envelope protein"
FT mat_peptide 2424..3479
FT /*tag= g
FT /product= "NS1 protein"
FT mat_peptide 3480..4133
FT /*tag= h
FT /product= "NS2A protein"
FT mat_peptide 4134..4523
FT /*tag= i
FT /product= "NS2B protein"
FT mat_peptide 4524..8377
FT /*tag= j
FT /product= "NS3 protein"
FT mat_peptide 6378..6758
FT /*tag= k
FT /product= "NS4A protein"
FT mat_peptide 6638..7562
FT /*tag= m
FT /product= "NS4B protein"
FT mat_peptide 6759..6827
FT /*tag= l
FT /product= "NS5 protein"
FT mat_peptide 7563..10262
FT /*tag= n
FT /product= "NS5 protein"
XX
XX WO200295075-A1.
XX
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-US016308.
XX
XX 22-MAY-2001; 2001US-0293049P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA (BLAN/) BLANEY J E.
XX
XX Whitehead SS, Murphy BR, Hanley KA;
XX
XX WPI; 2003-120809/11.
XX P-PSDB; AAE35313.
XX
XX New mutated flavivirus, useful for fine tuning the attenuation and growth
XX PT characteristics of dengue virus vaccines for the prevention and/or
XX PT treatment of dengue virus infection.
XX
XX Disclosure; Page 131-132; 246pp; English.
XX
XX The present invention relates to novel mutated flaviviruses comprising a
XX CC phenotype in which the viral genome is modified by introduction of a
XX CC mutation, singly or in combination, taken from mutations from recombinant
XX CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
XX CC mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
XX CC dengue type 4 virus. The methods and compositions of the invention are
XX CC useful for fine tuning the attenuation and growth characteristics of
XX CC dengue virus vaccines for the prevention and/or treatment of dengue virus
XX CC infection. The present sequence is Dengue virus type 4 strain rDEN4 DNA
XX
XX Sequence 10649 BP; 3298 A; 2214 C; 2804 G; 2333 T; 0 U; 0 Other;
XX

```

```
Query Match      100.0%; Score 28; DB 7; Length 10649;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AATATGCTGAACCGCGAGAGAAACCGCG 28
      |||||
Db      138 AATATGCTGAACCGCGAGAGAAACCGCG 165

RESULT 9
AAD53910
ID      AAD53910 standard; DNA; 10649 BP.
XX
AC      AAD53910;
XX
DT      28-MAY-2003 (first entry)
XX
DE      Dengue virus type 4 strain 2A DNA.
XX
KW      Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX
OS      Dengue virus.
XX
FH      Key      Location/Qualifiers
FT      CDS      102..10649
FT      /*tag= a
FT      /product= "DEN4 strain 2A protein"
FT      mat_peptide 102..440
FT      /*tag= c
FT      /product= "Anchored capsid protein"
FT      mat_peptide 102..398
FT      /*tag= b
FT      /product= "Virion capsid protein"
FT      mat_peptide 441..938
FT      /*tag= d
FT      /product= "Membrane precursor protein"
FT      mat_peptide 714..938
FT      /*tag= e
FT      /product= "Membrane protein"
FT      mat_peptide 939..2423
FT      /*tag= f
FT      /product= "Envelope protein"
FT      mat_peptide 2424..3479
FT      /*tag= g
FT      /product= "NS1 protein"
FT      mat_peptide 3480..4133
FT      /*tag= h
FT      /product= "NS2A protein"
FT      mat_peptide 4134..4523
FT      /*tag= i
FT      /product= "NS2B protein"
FT      mat_peptide 4524..6377
FT      /*tag= j
FT      /product= "NS3 protein"
FT      mat_peptide 6378..6758
FT      /*tag= k
FT      /product= "NS4A protein"
FT      mat_peptide 6759..6827
FT      /*tag= l
FT      /product= "2K protein"
FT      mat_peptide 6828..7562
FT      /*tag= m
FT      /product= "NS4B protein"
FT      mat_peptide 7563..10262
FT      /*tag= n
FT      /product= "NS5 protein"
XX
WO200295075-A1.
PN
28-NOV-2002.
XX
22-MAY-2002; 2002WO-US016308.
XX

22-MAY-2001; 2001US-0293049P.
XX
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (BLAN/) BLANEY J E.
XX
Whitehead SS, Murphy BR, Hanley KA;
XX
WPI; 2003-120809/11.
DR P-PSDB; AAE35312.
XX
New mutated flavivirus, useful for fine tuning the attenuation and growth
characteristics of dengue virus vaccines for the prevention and/or
treatment of dengue virus infection.
XX
Disclosure; Page 123-126; 246pp; English.
XX
The present invention relates to novel mutated flaviviruses comprising a
phenotype in which the viral genome is modified by introduction of a
mutation, singly or in combination, taken from mutations from recombinant
virus bearing Vero adaptation mutations, putative Vero cell adaptation
mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
dengue type 4 virus. The methods and compositions of the invention are
useful for fine tuning the attenuation and growth characteristics of
dengue virus vaccines for the prevention and/or treatment of dengue virus
infection. The present sequence is Dengue virus type 4 strain 2A DNA
XX
SQ      Sequence 10649 BP; 3302 A; 2212 C; 2800 G; 2335 T; 0 U; 0 Other;

Query Match      100.0%; Score 28; DB 7; Length 10649;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AATATGCTGAACCGCGAGAGAAACCGCG 28
      |||||
Db      138 AATATGCTGAACCGCGAGAGAAACCGCG 165

RESULT 10
AAD14605
ID      AAD14605 standard; cDNA; 10717 BP.
XX
AC      AAD14605;
XX
DT      11-SEP-2003 (revised)
DT      01-NOV-2001 (first entry)
XX
DE      Dengue virus (DEN)-2/3-VP1 chimeric cDNA.
XX
KW      Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
OS      Dengue virus; type II.
OS      Dengue virus; type III.
XX
FH      Key      Location/Qualifiers
FT      CDS      97..10266
FT      /*tag= a
FT      /product= "DEN-2/3-VP1 fusion protein"
XX
WO200160847-A2.
XX
23-AUG-2001.
XX
16-FEB-2001; 2001WO-US005142.
XX
16-FEB-2000; 2000US-0182829P.
XX
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
```



```
DR WPI: 2001-497162/54.
DR P-PSDB; AAE07984.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
PT
XX Example 2; Page 203-219; 470pp; English.
XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present CDNA
CC sequence encodes dengue virus (DEN)-2/3-VPI fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC premembrane/membrane protein (prM) and an envelope protein (E) from wild-
CC type DEN-3 16582 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10717 BP; 3501 A; 2208 C; 2737 G; 2271 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 4; Length 10717;
Best Local Similarity 100.0%; Pred.No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 136 AATATGCTGAAACGCGAGAGAAACCGCG 163

RESULT 11
AAQ12787
ID AAQ12787 standard; RNA; 10723 BP.
XX
AC AAQ12787;
XX
DT 25-MAR-2003 (revised)
DT 21-NOV-1991 (first entry)
XX
DE Dengue 2 virus genome.
XX
KW dengue virus; detection; consensus sequence; Flavivirus; PCR; ss.
XX
OS Dengue virus.
XX
FH Key Location/Qualifiers
FT CDS 97..10272
FT FT /tag= a
FT mat_peptide 712..936
FT /tag= b
FT /product= "M protein"
FT mat_peptide 937..2421
FT /tag= c
FT /product= "E protein"
FT mat_peptide 2422..3477
FT /tag= d
FT /product= "NS1"
FT mat_peptide 3478..4131
FT /tag= e
FT /product= "NS2A"
FT mat_peptide 4132..4518
FT /tag= f
FT /product= "NS2B"
FT mat_peptide 4519..6375
FT /tag= g
FT /product= "NS3"
```

```
FT mat_peptide 6376..6825
FT /tag= h
FT /product= "NS4a"
FT mat_peptide 6826..7569
FT /tag= i
FT /product= "NS4B"
FT mat_peptide 7570..10269
FT /tag= j
FT /product= "NS5"
XX
PN FR2654113-A.
XX
PD 10-MAY-1991.
XX
PF 09-NOV-1989; 89FR-00914724.
XX
PR 09-NOV-1989; 89PR-00014724.
XX
PA (INSP ) INST PASTEUR.
XX
XX Vincent D;
PI
XX WPI: 1991-225002/31.
DR P-PSDB; AAR13166.
XX
PT Detection and identification of Flaviviridae in biological sample - by
PT amplifying consensus sequence then hybridisation opt. followed by typing,
PT e.g. sequencing amplified prod.
XX
PS Disclosure; Fig 3; 24pp; French.
XX
CC The dengue 2 virus is an example of a member of the Flaviviridae which
CC can be identified using the probe pair of the invention. A species-
CC specific sequence can be amplified using the claimed oligonucleotides as
CC primers in a PCR reaction (see AAQ12788 and AAQ12789). Other viruses
CC which can be identified include Japanese encephalitis virus and yellow
CC fever virus. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 10723 BP; 3557 A; 2251 C; 2647 G; 3 T; 2249 U; 16 Other;
Query Match 100.0%; Score 28; DB 2; Length 10723;
Best Local Similarity 89.3%; Pred.No. 0.011;
Matches 25; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 136 AAUAUGUGAAACGCGAGAGAAACCGCG 163

RESULT 12
AAT49303
ID AAT49303 standard; CDNA; 10723 BP.
XX
AC AAT49303;
XX
DT 27-AUG-2003 (revised)
DT 11-SEP-1997 (first entry)
XX
DE cDNA sequence encoding polyprotein of DEN-2 virus, strain 16681.
XX
KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
KW DHF; DSS; ss.
XX
OS Dengue virus type 2 (strain 16681).
XX
FH Key Location/Qualifiers
FT CDS 97..10272
FT FT /tag= a
FT /product= "DEN-2 polyprotein"
FT /transl_except (pos:9208..9210, aa:Xaa)"
```

```

FT XX /note= "Xaa = unknown amino acid"
PN WO9640933-A1.
XX
XX
PD 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US009209.
XX
XX 07-JUN-1995; 95US-00483292.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
XX Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
XX Kinney R, Trent DW;
XX
XX WPI; 1997-052330/05.
XX P-PSDB; AAW06590.
XX
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
XX also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
XX quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Claim 23; Page 107-121; 261pp; English.
XX
XX This sequence encodes the polyprotein from Dengue 2 virus, strain 16681.
XX The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3,
XX NS4A, NS4B and NS5 proteins. A clone of this wildtype viral sequence, PDK
XX -53, may be used in the production of a quadravalent vaccine which
XX provides immunity against all four serotypes of dengue virus. The vaccine
XX also comprises a chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or
XX a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to
XX protect against infection by all four serotypes of dengue virus, DEN-1,
XX DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue
XX haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used
XX to produce the recombinant protein products of the DNA constructs which
XX are used in the vaccines. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2255 T; 0 U; 2 Other;
XX
XX Query Match 100.0%; Score 28; DB 2; Length 10723;
XX Best Local Similarity 100.0%; Pred. No. 0.011;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
XX |||||
XX Db 136 AATATGCTGAACGCGAGAGAAACCGCG 163
XX
XX RESULT 13
XX AAT49304
XX ID AAT49304 standard; cDNA; 10723 BP.
XX
XX AC AAT49304;
XX
XX XX
XX 27-AUG-2003 (revised)
XX 12-SEP-1997 (first entry)
XX
XX cDNA encoding polyprotein of attenuated DEN-2 virus, PDK-53.
XX
XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
XX NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
XX chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
XX dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
XX DHF; DSS; ss.
XX
XX Dengue virus type 2 (strain 16681).
XX Synthetic.
XX
XX Key Location/Qualifiers
XX mutation 57
XX FT /*tag= b
XX FT /note= "C>T mutation"

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CDS
FT 97. .10272
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FT /product= "DEN-2 attenuated polyprotein
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FT /transl_except(pos:1135. .1137, aa:Xaa)
FT /transl_except(pos:1393. .1395, aa:Xaa)
FT /transl_except(pos:2809. .2811, aa:Xaa)
FT /transl_except(pos:3040. .3042, aa:Xaa)
FT /transl_except(pos:9208. .9210, aa:Xaa)"
FT /note= "Xaa = unknown amino acid"
FT 524
FT mutation
FT /*tag= c
FT /note= "A>T mutation, causes Asp to Val substitution"
FT 2055
FT mutation
FT /*tag= d
FT /note= "C>T mutation"
FT 2579
FT mutation
FT /*tag= e
FT /note= "G>A mutation, causes Gly to Asp substitution"
FT 4018
FT mutation
FT /*tag= f
FT /note= "C>T mutation, causes Leu to Phe substitution"
FT 5547
FT mutation
FT /*tag= g
FT /note= "C>T mutation"
FT 6599
FT mutation
FT /*tag= h
FT /note= "G>C mutation, causes Gly to Ala substitution"
FT 8571
FT mutation
FT /*tag= i
FT /note= "C>T mutation"
XX
XX WO9640933-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US009209.
XX
XX 07-JUN-1995; 95US-00483292.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
XX Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
XX Kinney R, Trent DW;
XX
XX WPI; 1997-052330/05.
XX P-PSDB; AAW06591.
XX
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
XX also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
XX quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Claim 27; Page 122-136; 261pp; English.
XX
XX This sequence encodes the polyprotein from an attenuated derivative of
XX Dengue 2 virus, strain 16681. The derivative is designated PDK-53. The
XX polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A,
XX NS4B and NS5 proteins. The PDK-53 viral sequence may be used in the
XX production of a quadravalent vaccine which provides immunity against all
XX four serotypes of dengue virus. The vaccine also comprises a chimeric
XX DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus.
XX The new quadravalent vaccines are used to protect against infection by
XX all four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and DEN-4, which
XX can lead to dengue fever or fatal dengue haemorrhagic fever/dengue shock
XX syndrome (DHF/DSS). Host cells are used to produce the recombinant
XX protein products of the DNA constructs which are used in the vaccines.
XX (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 10723 BP; 3548 A; 2196 C; 2711 G; 2261 T; 0 U; 7 Other;
XX
XX Query Match 100.0%; Score 28; DB 2; Length 10723;
XX Best Local Similarity 100.0%; Pred. No. 0.011;

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Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity	100.0%;	Pred. No. 0.011;	
Matches 28;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps 0;			

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | |
Db 136 AATATGCTGAAACGCGAGAGAAACCGCG 163

Search completed: August 3, 2004, 18:46:03
Job time : 154.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 18:28:49 ; Search time 37 Seconds
(without alignments)
419.963 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28
Sequence: 1 aaatgctgaacgcgagagaaacgcg 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/2/ina/5A COMB.seq:
2: /cgn2_6/prodata/2/ina/5B COMB.seq:
3: /cgn2_6/prodata/2/ina/6A COMB.seq:
4: /cgn2_6/prodata/2/ina/6B COMB.seq:
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq:
6: /cgn2_6/prodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	2357	4	US-08-869-423-1
2	28	100.0	3381	3	US-08-937-195-1
3	28	100.0	3381	3	US-08-937-195-2
4	28	100.0	3381	3	US-08-915-152-1
5	28	100.0	3381	3	US-08-915-152-2
6	28	100.0	3381	5	PCT-US96-07627-1
7	28	100.0	3381	5	PCT-US96-07627-2
8	26.4	94.3	10718	3	US-08-325-426B-1
9	18.4	65.7	1443	3	US-09-078-173A-11
10	18.4	65.7	4512	1	US-08-224-391-52
11	18.4	65.7	4512	1	US-08-484-304-52
12	18.4	65.7	12980	3	US-08-911-566-5
13	18.4	65.7	12980	4	US-09-034-756-5
14	17.4	62.1	993	3	US-08-875-233-11
15	17.4	62.1	1227	4	US-09-328-352-1888
16	17.4	62.1	2646	4	US-09-221-017B-558
17	17.4	62.1	5026	4	US-09-549-872B-5
18	17.4	62.1	6612	4	US-09-549-872B-5
19	17.4	62.1	11207	4	US-09-549-872B-2
20	17.2	61.4	3243	1	US-08-611-107-32
21	17.2	61.4	24358	4	US-09-392-812A-1
22	17	60.7	435	4	US-09-252-991A-1169
23	17	60.7	2355	4	US-08-913-159-12
24	17	60.7	2409	4	US-09-252-991A-1259
25	17	60.7	3378	4	US-09-328-352-4107
26	16.8	60.0	287	4	US-09-313-294A-1156
27	16.8	60.0	936	4	US-09-252-991A-11497

c	28	16.8	60.0	1746	4	US-09-489-039A-6977	Sequence 6977, Ap
	29	16.6	59.3	297	4	US-09-313-294A-522	Sequence 522, App
	30	16.6	59.3	702	4	US-08-956-171E-314	Sequence 314, App
	31	16.6	59.3	792	4	US-09-134-000C-295	Sequence 295, App
	32	16.6	59.3	851	4	US-08-961-527-361	Sequence 361, App
	33	16.6	59.3	2558	4	US-08-936-165A-214	Sequence 214, App
	34	16.6	59.3	10091	3	US-09-058-483-34	Sequence 34, Appl
	35	16.4	58.6	652	4	US-09-221-017B-105	Sequence 105, App
	36	16.4	58.6	1404	4	US-09-620-312D-710	Sequence 710, App
	37	16.4	58.6	1579	4	US-09-591-095-9	Sequence 9, Appli
	38	16.4	58.6	4008	4	US-09-976-594-158	Sequence 158, App
	39	16.2	57.9	493	4	US-09-439-313-450	Sequence 450, App
	40	16.2	57.9	493	4	US-09-352-618A-450	Sequence 450, App
	41	16.2	57.9	493	4	US-09-636-215-450	Sequence 450, App
	42	16.2	57.9	493	4	US-09-685-166A-450	Sequence 450, App
	43	16.2	57.9	730	3	US-09-328-111-693	Sequence 693, App
	44	16.2	57.9	3747	4	US-09-690-364-17	Sequence 17, Appl
	45	16.2	57.9	7042	3	US-09-092-508-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-869-423-1
; Sequence 1, Application US/08869423
; Patent No. 6455509
; GENERAL INFORMATION:
; APPLICANT: Kochel, Tadeusz
; APPLICANT: Porter, Kevin R.
; APPLICANT: Raviprakash, Kanakatte
; APPLICANT: Hoffmann, Stephen L.
; APPLICANT: Hayes, Curtis G.
; TITLE OF INVENTION: Dengue Nucleic Acid Vaccines that Induce
; TITLE OF INVENTION: Neutralizing Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Naval Medical Res. & Dev. Cmd.
; STREET: 8901 Wisconsin Ave., Bldg. 1, T-12
; CITY: Bethesda
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20889-5606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,423
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,839
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kalish, Daniel
; REGISTRATION NUMBER: 33,599
; REFERENCE/DOCKET NUMBER: NC 77,654
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 295-5642
; TELEFAX: (301) 295-1022
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:

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; ORGANISM: Dengue virus
; STRAIN: New Guinea C
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Prem and Envelope
; MAP POSITION: 330-2446
; UNITS: bp
; PUBLICATION INFORMATION:
; AUTHORS: Gruenberg, A
; AUTHORS: Woo, W S
; AUTHORS: Biedrzycka, A
; AUTHORS: Wright, P J
; TITLE: Partial nucleotide sequence and deduced amino
; TITLE: acid sequence of the structural proteins of dengue
; TITLE: virus type 2, New Guinea C and PUO-218 strains
; JOURNAL: J. Gen. Virol.
; VOLUME: 69
; PAGES: 1391-1398
; DATE: 1988
; PUBLICATION INFORMATION:
; AUTHORS: Irie, K
; AUTHORS: Mohan, P M
; AUTHORS: Sasaguri, Y
; AUTHORS: Putnak, R
; AUTHORS: Padmanabhan, R
; TITLE: Sequence Analysis of Cloned dengue virus type
; TITLE: 2 genome (New Guinea-C strain)
; JOURNAL: Gene
; VOLUME: 75
; ISSUE: 2
; PAGES: 197-211
; DATE: 1989
; PUBLICATION INFORMATION:
; AUTHORS: Yaegashi, T
; AUTHORS: Vakharia, V N
; AUTHORS: Page, K
; AUTHORS: Sasaguri, Y
; AUTHORS: Feighny, R
; AUTHORS: Padmanabhan, R
; JOURNAL: Gene
; VOLUME: 46
; ISSUE: 2-3
; PAGES: 257-267
; DATE: 1986
;
US-08-869-423-1
Query Match 100.0%; Score 28; DB 4; Length 2357;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 60 AATATGCTGAAACGCGAGAGAAACCGCG 87

RESULT 2
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; Sequence 1, Application US/08937195
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,195
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/488,807
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PRI59/S1
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: /note= "Positions in the S1 strain
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; OTHER INFORMATION: reported by Hahn(Citation #1)"
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; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1260
; OTHER INFORMATION: /note= "T is replaced by G for
; OTHER INFORMATION: Wild-Type sequence"
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; LOCATION: 1762
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; LOCATION: 1929
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; LOCATION: 2310
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"

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; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
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; LOCATION: 841
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; OTHER INFORMATION: sequence for Envelope"
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; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
;
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
;
; US-08-937-195-1
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; Query Match 100.0%; Score 28; DB 3; Length 3381;
; Best Local Similarity 100.0%; Pred. No. 0.00091;
; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
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;
; Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67
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; RESULT 3
; US-08-937-195-2
; Sequence 2, Application US/08937195
; Patent No. 6136561
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,195
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/488,807
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid

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;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (DEN-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
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; NAME/KEY: CDS
; LOCATION: 1..3381
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1216..1218
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; OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR159;
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= (11)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1258..1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; OTHER INFORMATION: replaced for GTT(coding for Val) for the wild-type DEN-2 PR159;
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; OTHER INFORMATION: /citation= (11)
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; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= (11)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
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; US-08-937-195-2
;
; Query Match 100.0%; Score 28; DB 3; Length 3381;

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Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 4
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; Sequence 1, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,152
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,469
; FILING DATE: 10-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: group(103, 1940, 1991, 2025)
; OTHER INFORMATION: /note= "Positions in the S1 strain
; OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
; OTHER INFORMATION: reported by Hahn(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1218
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1260
; OTHER INFORMATION: /note= "T is replaced by G for
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; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1929
; OTHER INFORMATION: /note= "C is replaced by T for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2310
; OTHER INFORMATION: /note= "A is replaced by N for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; US-08-915-152-1

Query Match 100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
    |||||
Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 5
US-08-915-152-2
; Sequence 2, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
```


COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-AUG-1997
CLASSIFICATION: 435
PRIORITY APPLICATION NUMBER: US 08/500,469
FILING DATE: 10-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.21
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (DEN-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3381
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1216..1218
OTHER INFORMATION: /note= "GAG(coding for Glu) is
OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1258..1260
OTHER INFORMATION: /note= "GTG(coding for Val) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1762..1764
OTHER INFORMATION: /note= "ATT(coding for Ile) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1927..1929
OTHER INFORMATION: /note= "ACT(Coding for Ser) is
OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Capsid"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 343

OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for preMembrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Membrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Envelope"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
PAGES: 167-180
DATE: 1988
US-08-915-152-2
Query Match 100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. NO. 0.00091;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGGAGAGAAACCGCG 28
DB 40 AATATGCTGAAACGGAGAGAAACCGCG 67
RESULT 6
PCT-US96-07627-1
Sequence 1, Application PC/TUS9607627
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
NUMBER OF SEQUENCES: 50
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07627
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (Den-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FEATURE:
NAME/KEY: misc_feature
LOCATION: group(103, 1940, 1991, 2025)
OTHER INFORMATION: /note= "Positions in the S1 strain
OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
OTHER INFORMATION: reported by Hahn(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1218
OTHER INFORMATION: /note= "G is replaced by A for
OTHER INFORMATION: Wild-Type sequence"
FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: 1260_
; OTHER INFORMATION: /note= "T is replaced by G for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762_
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1929_
; OTHER INFORMATION: /note= "C is replaced by T for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2310_
; OTHER INFORMATION: /note= "A is replaced by N for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1_
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343_
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616_
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841_
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326_
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; PCT-US96-07627-1
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Query Match 100.0%; Score 28; DB 5; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AATATGCTGAACCGAGAGAACCGCG 28
Db 40 AATATGCTGAACCGAGAGAACCGCG 67
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RESULT 7
PCT-US96-07627-2
; Sequence 2, Application PC/TUS9607627
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2(DEN-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PRI59/S1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3381
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1216_-1218
; OTHER INFORMATION: /note= "GAG(coding for Glu) is
; OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PRI5:
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1258_-1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PRI5:
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762_-1764
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PRI59
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1927_-1929
; OTHER INFORMATION: /note= "AGT(Coding for Ser) is
; OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PRI59
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1_
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343_
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616_
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841_
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326_
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
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; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
PCT-US96-07627-2

Query Match      100.0%; Score 28; DB 5; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGGAGAGAAACCGCG 28
    |||||
Db 40 AATATGCTGAACGCGGAGAGAAACCGCG 67

RESULT 8
US-08-325-426B-1
; Sequence 1, Application US/08325426B
; Patent No. 6017535
; GENERAL INFORMATION:
; APPLICANT: FU, Jianlin
; APPLICANT: TAN, Boon-Haun
; APPLICANT: YAP, Eu-Hian
; APPLICANT: CHAN, Yow-Cheong
; APPLICANT: TAN, Yin-Hwee
; TITLE OF INVENTION: CDNA SEQUENCE OF DENGUE VIRUS SEROTYPE 1
; TITLE OF INVENTION: (SINGAPORE STRAIN)
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON and VANDERHYE PC
; STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,426B
; FILING DATE: 16-DEC-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10718 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA sequence corresponding to
; MOLECULE TYPE: the genomic RNA of DEN1-S275/90
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Dengue Fever Virus Type 1
; STRAIN: S275/90
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 81..10268
US-08-325-426B-1

Query Match      94.3%; Score 26.4; DB 3; Length 10718;
Best Local Similarity 96.4%; Pred. No. 0.0063;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGGAGAGAAACCGCG 28
    |||||
Db 120 AATATGCTGAACGCGGAGAGAAACCGCG 147

RESULT 9
US-09-078-173A-11
; Sequence 11, Application US/09078173A
; Patent No. 6200794

; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskins
; APPLICANT: Alan Braeh
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; TITLE OF INVENTION: LYASE AND USES THEREOF
; FILE REFERENCE: 06027.0001
; CURRENT APPLICATION NUMBER: US/09/078,173A
; CURRENT FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annuum (green pepper)
US-09-078-173A-11

Query Match      65.7%; Score 18.4; DB 3; Length 1443;
Best Local Similarity 78.6%; Pred. No. 21;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGGAGAGAAACCGCG 28
    |||||
Db 933 AATATGCTGAGATGCAAGAGAAACTGAG 960

RESULT 10
US-08-224-391-52
; Sequence 52, Application US/08224391
; Patent No. 5744140
; GENERAL INFORMATION:
; APPLICANT: Paolletti, Enzo
; APPLICANT: Pincus, Steven E.
; TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,391
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/729,800
; FILING DATE: 17-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2340
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4512 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-224-391-52

Query Match      65.7%; Score 18.4; DB 1; Length 4512;
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TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-034-756-5

Query Match 65.7%; Score 18.4; DB 4; Length 12980;
Best Local Similarity 78.6%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGGCGAGAGAAACCGCG 28
DB 9714 AATATGCTAAACGGCGGATACCCCGCG 9687

RESULT 14
US-08-875-233-11
; Sequence 11, Application US/08875233
; Patent No. 6127601
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; APPLICANT: McMaster, J. Russell
; APPLICANT: Tricoli, David M
; APPLICANT: Reynolds, John F
; APPLICANT: Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; TITLE OF INVENTION: Cucumber Mosaic Virus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60689
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 983 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: CUCUMBER MOSAIC VIRUS
; STRAIN: WHITE LEAF
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..657
; PUBLICATION INFORMATION:

AUTHORS: Quemada, H
AUTHORS: Kearney, C
AUTHORS: Gonsalves, D
AUTHORS: Slightom, J
TITLE: Nucleotide Sequences of the Coat Protein
TITLE: Genes and Flanking Regions of Cucumber Mosaic
TITLE: Virus Strains C and WL RNA 3
JOURNAL: J. Gen. Virol.
VOLUME: 70
PAGES: 1065-1073
DATE: 1989
US-08-875-233-11

Query Match 62.1%; Score 17.4; DB 3; Length 983;
Best Local Similarity 77.8%; Pred. No. 56;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGGCGAGAGAAACCGCG 28
DB 113 AGATGCTGAAACTCAATAGAACCTCG 139

RESULT 15
US-09-328-352-1888/c
; Sequence 1888, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1888
; LENGTH: 1227
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1888

Query Match 62.1%; Score 17.4; DB 4; Length 1227;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGGCGAGAGAAACCGCG 27
DB 964 AATATGCAAAACCGAAGAGAAACCGCG 938

Search completed: August 3, 2004, 19:52:13
Job time : 38 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
868.911 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatattgctgaacgcgagagaaacccgcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
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- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	28	14	US-10-085-944-2
2	28	100.0	3381	15	US-10-247-960-2
3	26	92.9	26	9	US-09-840-707A-23
4	26	92.9	26	15	US-10-038-557A-23
5	18.8	67.1	1428	16	US-10-369-493-32952
6	18.6	66.4	1602	15	US-10-156-761-2266
7	18.6	66.4	9025608	15	US-10-156-761-1
8	18.4	65.7	1443	14	US-10-042-991-11
9	18.4	65.7	12980	9	US-09-238-076-5
10	18.4	65.7	12980	10	US-09-995-937-5
11	18.4	65.7	12980	10	US-09-917-563-5
12	18.2	65.0	452	10	US-09-918-995-27460
13	18.2	65.0	2179	13	US-09-823-245A-434
14	18.2	65.0	9875	10	US-09-764-891-7878

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15 17.6 62.9 529 13 US-10-424-599-130933 Sequence 130933,
16 17.6 62.9 550 15 US-10-198-846-11819 Sequence 11819, A
17 17.6 62.9 838 15 US-10-198-846-3468 Sequence 3468, Ap
18 17.6 62.9 945 16 US-10-398-221-2508 Sequence 2508, Ap
19 17.6 62.9 945 16 US-10-398-221-2571 Sequence 2571, Ap
20 17.6 62.9 966 16 US-10-398-221-553 Sequence 553, App
21 17.6 62.9 966 16 US-10-398-221-554 Sequence 554, App
22 17.6 62.9 1646 13 US-10-282-122A-29374 Sequence 29374, A
23 17.6 62.9 9718 8 US-08-319-974A-1 Sequence 1, Appli
24 17.6 62.9 684707 16 US-10-398-221-9 Sequence 9, Appli
25 17.6 62.9 684707 16 US-10-398-221-9 Sequence 9, Appli
26 17.6 62.9 3011208 16 US-10-398-221-2058 Sequence 2058, Ap
27 17.4 62.1 379 10 US-09-738-269-20 Sequence 20, Appl
28 17.4 62.1 379 14 US-10-023-437-20 Sequence 20, Appl
29 17.4 62.1 382 17 US-10-437-963-17200 Sequence 17200, A
30 17.4 62.1 528 13 US-10-424-599-53946 Sequence 53946, A
31 17.4 62.1 558 13 US-10-027-632-237136 Sequence 237136,
32 17.4 62.1 558 16 US-10-027-632-237136 Sequence 237136,
33 17.4 62.1 774 13 US-10-282-122A-39862 Sequence 39862, A
34 17.4 62.1 778 13 US-10-282-122A-36749 Sequence 36749, A
35 17.4 62.1 983 14 US-10-011-033-11 GENERAL INFORMA
36 17.4 62.1 2520 10 US-09-738-269-22 Sequence 22, Appl
37 17.4 62.1 2520 14 US-10-023-437-22 Sequence 22, Appl
38 17.4 62.1 2646 13 US-10-194-163-558 Sequence 558, App
39 17.4 62.1 2784 17 US-10-437-963-21921 Sequence 21921, A
40 17.4 62.1 5026 15 US-10-371-101-3 Sequence 3, Appli
41 17.4 62.1 5026 15 US-10-371-101-5 Sequence 5, Appli
42 17.4 62.1 11207 15 US-10-371-101-2 Sequence 2, Appli
43 17.4 62.1 39726 15 US-10-309-933-1 Sequence 1, Appli
44 17.4 62.1 145068 17 US-10-322-281-33 Sequence 33, Appli
45 17.4 62.1 235070 13 US-10-087-192-1990 Sequence 1990, Ap

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ALIGNMENTS

```

RESULT 1
US-10-085-944-2
; Sequence 2, Application US/10085944
; Publication No. US20020155435A1
; GENERAL INFORMATION:
; APPLICANT: Wang Wei-Kung
; TITLE OF INVENTION: DETECTION OF DENGUE VIRUS
; FILE REFERENCE: 12563-004001
; CURRENT APPLICATION NUMBER: US/10/085,944
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/272,535
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-085-944-2

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Query Match 100.0%; Score 28; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAACCGGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | |
Db 1 AATATGCTGAACCGGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | |

```

```

RESULT 2
US-10-247-960-2
; Sequence 2, Application US/10247960
; Publication No. US20030175304A1
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.

```

; APPLICANT: Peters, Iain
; APPLICANT: Collier, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; TITLE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
; FILE REFERENCE: 24733-20005.01
; CURRENT APPLICATION NUMBER: US/10/247,960
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/376,463
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3381
; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-10-247-960-2

Query Match 100.0%; Score 28; DB 15; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.011; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACCGCGAGAGAAACCGCG 28
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DB 40 AATATGCTGAAACCGCGAGAGAAACCGCG 67
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RESULT 3
US-09-840-707A-23
; Sequence 23, Application US/09840707A
; Patent No. US20020077276A1
; GENERAL INFORMATION:
; APPLICANT: Fredeking, Terry M.
; APPLICANT: Ignatyev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
; FILE REFERENCE: 24881-301C
; CURRENT APPLICATION NUMBER: US/09/840,707A
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: upper primer for Dengue virus type 2 detection
US-09-840-707A-23

Query Match 92.9%; Score 26; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.046; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACCGCGAGAGAAACCG 26
|||||
DB 1 AATATGCTGAAACCGCGAGAGAAACCG 26
|||||

RESULT 4
US-10-038-557A-23
; Sequence 23, Application US/10038557A

; Publication No. US20030092684A1
; GENERAL INFORMATION:
; APPLICANT: Fredeking, Terry M.
; APPLICANT: Ignatyev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
; FILE REFERENCE: 24881-301D
; CURRENT APPLICATION NUMBER: US/10/038,557A
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 09/840,707
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: upper primer for Dengue virus type 2 detection
US-10-038-557A-23

Query Match 92.9%; Score 26; DB 15; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.046; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACCGCGAGAGAAACCG 26
|||||
DB 1 AATATGCTGAAACCGCGAGAGAAACCG 26
|||||

RESULT 5
US-10-369-493-32952/c
; Sequence 32952, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 32952
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-369-493-32952

Query Match 67.1%; Score 18.8; DB 16; Length 1428;
Best Local Similarity 90.9%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTGAAACCGCGAGAGAAACCGCG 28
|||||
DB 1184 CGGAACCGCGAGAGAAACCGCG 1163
|||||

RESULT 6
US-10-156-761-2266
; Sequence 2266, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:


```

; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2266
; TYPE: DNA
; LENGTH: 1602
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1602)
US-10-156-761-2266

Query Match          66.4%; Score 18.6; DB 15; Length 1602;
Best Local Similarity 84.0%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ATGCTGACCGCGAGAGAACCGCG 28
Db 115 AAGCTGACCGCGAGAGAACCGCG 139
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RESULT 7
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match          66.4%; Score 18.6; DB 15; Length 9025608;
Best Local Similarity 84.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ATGCTGACCGCGAGAGAACCGCG 28
Db 2778649 AAGCTGACCGCGAGAGAACCGCG 2778625
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RESULT 8
US-10-042-991-11
; Sequence 11, Application US/10042991
; Publication No. US20020142407A1
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskin
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; TITLE OF INVENTION: LYASE AND USES THEREOF
; FILE REFERENCE: 06027.000103
; CURRENT APPLICATION NUMBER: US/10/042,991
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annum (green pepper)
US-10-042-991-11

Query Match          65.7%; Score 18.4; DB 14; Length 1443;
Best Local Similarity 78.6%; Pred. No. 2.2e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAACCGCG 28
Db 933 AAATGCTGAGATGCAAGAGAACTGAG 960

RESULT 9
US-09-238-076-5/c
; Sequence 5, Application US/09238076
; Patent No. US20020102540A1
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
; TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/238,076
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/034,756
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
US-09-238-076-5

Query Match 65.7%; Score 18.4; DB 9; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||||
Db 9714 AATATGCTAAAACCGGCATACCCCGCG 9687

RESULT 10
US-09-995-937-5/c
/ Sequence 5, Application US/09995937
/ Publication No. US20030028010A1
/ GENERAL INFORMATION:
/ APPLICANT: RICE, CHARLES et al.
/ TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
/ VIRUS (HCV) AND USES THEREOF
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: HOWELL & HAFERKAMP, L.C.
/ STREET: 7733 FORSYTH BLVD., SUITE 1400
/ CITY: ST. LOUIS
/ STATE: MO
/ COUNTRY: USA
/ ZIP: 63105
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/995,937
/ FILING DATE: 04-May-1998
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/034,756
/ FILING DATE: 04-May-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: HOLLAND, DONALD R.
/ REGISTRATION NUMBER: 35,197
/ REFERENCE/DOCKET NUMBER: 6029-4831
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 314-727-5188
/ TELEFAX: 314-727-6092
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12980 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-995-937-5

Query Match 65.7%; Score 18.4; DB 10; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||||
Db 9714 AATATGCTAAAACCGGCATACCCCGCG 9687

RESULT 11
US-09-917-563-5/c
/ Sequence 5, Application US/09917563
/ Publication No. US20030073080A1
/ GENERAL INFORMATION:
/ APPLICANT: RICE, CHARLES et al.
/ TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
/ VIRUS (HCV) AND USES THEREOF
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: HOWELL & HAFERKAMP, L.C.
/ STREET: 7733 FORSYTH BLVD., SUITE 1400
/ CITY: ST. LOUIS
/ STATE: MO
/ COUNTRY: USA
/ ZIP: 63105
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/917,563
/ FILING DATE: 27-Jul-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/238,076
/ FILING DATE: 26-JAN-1999
/ ATTORNEY/AGENT INFORMATION:
/ NAME: HOLLAND, DONALD R.
/ REGISTRATION NUMBER: 35,197
/ REFERENCE/DOCKET NUMBER: 6029-4831
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 314-727-5188
/ TELEFAX: 314-727-6092
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12980 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-917-563-5

Query Match 65.7%; Score 18.4; DB 10; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||||
Db 9714 AATATGCTAAAACCGGCATACCCCGCG 9687

RESULT 12
US-09-918-995-27460
/ Sequence 27460, Application US/09918995
/ Publication No. US20030073623A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc.
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
/ FROM VARIOUS CDNA LIBRARIES
/ FILE REFERENCE: 20411-756
/ CURRENT APPLICATION NUMBER: US/09/918,995
/ CURRENT FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: US/09/235,076
/ PRIOR FILING DATE: 1999-01-20
/ NUMBER OF SEQ ID NOS: 38054
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 27460
/ LENGTH: 452
/ TYPE: DNA
/ ORGANISM: Homo sapiens
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Query Match	65.0%;	Score 18.2;	DB 10;	Length 9875;
Best Local Similarity	87.0%;	Pred. No. 3.6e+02;		

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 3, 2004, 18:26:44 ; Search time 1253 Seconds
(without alignments)
667.311 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatagtctgaacgcgagagaacgcg 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pig:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20.6	73.6	776	14	CF996467
2	19.8	70.7	720	14	CF455745
3	19.6	70.0	301	14	CB078143
4	19.6	70.0	712	14	CF372439

C	5	19.6	70.0	722	14	CF512147
C	6	19.6	70.0	734	14	CF512236
C	7	19.4	69.3	464	10	BE841207
C	8	19	67.9	559	29	TA262H01Q
C	9	19	67.9	568	28	AQ945692
C	10	19	67.9	576	29	TA140D12P
C	11	19	67.9	580	10	BE776235
C	12	19	67.9	602	9	AL673619
C	13	19	67.9	629	9	AL674632
C	14	19	67.9	633	14	CA349616
C	15	19	67.9	649	14	CA356841
C	16	19	67.9	768	29	CC504335
C	17	19	67.9	870	29	AG186531
C	18	19	67.9	988	14	CF995511
C	19	18.8	67.1	1687	10	BF128456
C	20	18.6	66.4	407	14	CF198531
C	21	18.6	66.4	456	12	BG659286
C	22	18.6	66.4	563	14	CF93381
C	23	18.6	66.4	584	28	AQ657703
C	24	18.6	66.4	593	29	FR0021761
C	25	18.6	66.4	642	9	AI135620
C	26	18.6	66.4	684	28	AQ657387
C	27	18.4	65.7	427	29	CG016439
C	28	18.4	65.7	456	28	AQ724090
C	29	18.4	65.7	496	10	AW592272
C	30	18.4	65.7	582	28	BZ130571
C	31	18.4	65.7	655	14	CB020289
C	32	18.4	65.7	672	28	BH100535
C	33	18.4	65.7	675	13	CA112278
C	34	18.4	65.7	695	28	BH929269
C	35	18.4	65.7	697	28	BH549312
C	36	18.4	65.7	743	14	CK326303
C	37	18.4	65.7	750	10	BE615972
C	38	18.4	65.7	774	28	BZ154086
C	39	18.4	65.7	788	28	BZ132164
C	40	18.4	65.7	790	10	BF678988
C	41	18.4	65.7	792	12	BI753870
C	42	18.4	65.7	824	10	BF620613
C	43	18.4	65.7	1101	29	CNS00KGJ
C	44	18.4	65.7	1126	9	AL697344
C	45	18.4	65.7	1253	10	BF690226

ALIGNMENTS

RESULT 1
CF996467/c
LOCUS
DEFINITION
AGENCY: NIH_ZGC_7
5', mRNA sequence.
ACCESSION
CF996467
VERSION
CF996467.1
KEYWORDS
EST:
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
REFERENCE
1 (bases 1 to 776)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

CF996467
AGENCY: NIH_ZGC_7
5', mRNA sequence.
ACCESSION
CF996467
VERSION
CF996467.1
KEYWORDS
EST:
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
REFERENCE
1 (bases 1 to 776)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Daniela S. Gerhard, Ph.D.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM14788 row: e column: 03
 High quality sequence stop: 734.

FEATURES

source
 1. .776
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:7037741"
 /tissue_type="whole body"
 /lab_host="DH10B"
 /clone_lib="NIH_ZGC 7"
 /notes="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
 Bulk tissue was collected from a whole adult individual
 from the Tuebingen strain. 1st strand cDNA was primed with
 a Not I - oligo(dT) primer, double-stranded cDNA was
 cloned into the Not I and EcoRV sites of pExpress-1.
 Library was size-selected for >1 kb fragments and
 normalized. A non-normalized version of this library is
 also available (NIH_ZGC10). Library was constructed by
 Open Biosystems (Huntsville, AL)"

ORIGIN
 Query Match 73.6%; Score 20.6; DB 14; Length 776;
 Best Local Similarity 85.2%; Pred. No. 1.7e+02;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAAACCGCG 28
 ||||||| ||||||| ||||||| |||||
 Db 549 ATGTGCTGACACGCGAGAGACCGAG 523

RESULT 2
 CF455745
 LOCUS
 DEFINITION AGENCOURT 15376947 Human Anterior Horn Homo sapiens cDNA clone
 IMAGE:30515857 5', mRNA sequence.
 ACCESSION CF455745
 VERSION CF455745.1 GI:34455401
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 720)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: gsapbe@mail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAMS81 row: k column: 02
 High quality sequence start: 194
 High quality sequence stop: 544.

FEATURES
 source
 1. .720
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30515857"
 /tissue_type="Peripheral Nervous system"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="Human Anterior Horn"

ORIGIN

Query Match 70.7%; Score 19.8; DB 14; Length 720;
 Best Local Similarity 91.3%; Pred. No. 3.7e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAA 23
 ||||||| ||||||| ||||||| |||||
 Db 189 AAGATGCTGAACACACGAGAGAAA 211

RESULT 3
 CB078143
 LOCUS
 DEFINITION H363h04.g1 Hedyotis terminalis flower - Stage 2 (NYBG) Hedyotis
 terminalis cDNA clone h363h04, mRNA sequence.

ACCESSION CB078143
 VERSION CB078143.1 GI:27891580
 KEYWORDS EST.
 SOURCE Hedyotis terminalis
 ORGANISM Hedyotis terminalis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiids; Gentianales; Rubiaceae; Rubioloideae;
 Spmacoceae; Hedyotis.
 1 (bases 1 to 301)
 Levesque, M.P., Twigg, R.W., Motley, T., Katari, M.S., Dedhia, N.N.,
 O'Shaughnessy, A.L., Ballja, V., Martienssen, R.A., McCombie, R.W.,
 Bentley, P. and Stevenson, D.
 Expressed tag sequences from Hedyotis terminalis flower - Stage 2
 (NYBG)

UNPUBLISHED

Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mccombie@cshl.org
 Plate: h363 row: h column: 04
 Seq primer: -21M13UnivRev
 High quality sequence stop: 301.

FEATURES

source
 1. .301
 /organism="Hedyotis terminalis"
 /mol_type="mRNA"
 /db_xref="taxon:219667"
 /clone="h363h04"
 /dev_stage="pre-anthesis; Stage 2"
 /clone_lib="Hedyotis terminalis flower - Stage 2 (NYBG)"
 /notes="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
 Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
 CHSL 12/21/01 Library: Strategene ZAP Express cDNA
 Synthesis Kit. The library was size-fractionated to enrich
 for large inserts. Sample: collected on the island of
 Hawaii, Hawaii; NYBG herbarium voucher TM2562"

ORIGIN

Query Match 70.0%; Score 19.6; DB 14; Length 301;
 Best Local Similarity 84.8%; Pred. No. 3.6e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TATGCTGAACGCGAGAGAAACCGCG 28
 ||||||| ||||||| ||||||| |||||
 Db 212 TATGCTGAACGCTGACAGAGCGCG 237

RESULT 4

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CF372439      712 bp      mRNA      linear      EST 27-AUG-2003
LOCUS      CSECS052D08_Flon0012 CabSau Normalised Flower Stage 12 (FLon0012)
DEFINITION      Vitis vinifera cDNA clone CSECS052D08 3', mRNA sequence.
ACCESSION      CF372439
VERSION      CF372439.1      GI:34319685
KEYWORDS      EST:
SOURCE      Vitis vinifera
ORGANISM      Vitis vinifera
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE      rosids; Vitaceae; Vitis.
JOURNAL      1 (bases 1 to 712)
COMMENT      Iocco, P., Hua, C., Davies, C. and Thomas, M.R.
              Expressed sequence tags from the grapevine cultivar Cabernet
              Sauvignon
              Unpublished (2003)
              Contact: Mark R. Thomas
              CSIRO Plant Industry
              CSIRO
              PO Box 350, Glen Osmond, SA, 5064, Australia
              Tel: 61 8 83038600
              Fax: 61 8 83038601
              Email: Mark.R.Thomas@csiro.au
              Seq primer: CCAGTCACGAGCTGTGTAAGC (M13 Forward)
              POLYA=Yes.
FEATURES      Location/Qualifiers
source      1..712
              /organism="Vitis vinifera"
              /mol_type="mRNA"
              /cultivar="Cabernet Sauvignon"
              /db_xref="taxon:29760"
              /clone="CSECS052D08"
              /sex="Hermaphrodite"
              /dev_stage="12 - modified E-L system"
              /clone_lib="CabSau Normalised Flower Stage 12 (FLon0012)"
              /note="Organ: Inflorescence including flowers; Vector:
              p2L; Normalised cDNA library from immature inflorescences
              at stage 12 of the modified E-L system. Tissue collected
              from field grown plants. A description of the modified E-L
              system can be found in the paper by B. G. Coombe 'Adoption
              of a system for identifying grapevine growth stages'
              (1995) Aust. J. Grape and Wine Res. 1: 104-110."
ORIGIN
Query Match      70.0%; Score 19.6; DB 14; Length 712;
Best Local Similarity      84.6%; Pred. No. 4.5e+02;
Matches      22; Conservative      0; Mismatches      4; Indels      0; Gaps      0;

QY      1      AATATGCTGAACGCGAGAGAAACCG 26
Db      374      ATTATGCTGAACCTCGAAGAAACTG 399

RESULT 5
CF512147/c      722 bp      mRNA      linear      EST 09-SEP-2003
LOCUS      Cabud0003_IF_A10 Vitis vinifera cv. cabernet sauvignon (Clone 8)
DEFINITION      Bud - CABUD Vitis vinifera cDNA clone Cabud0003_IF_A10 5', mRNA
              sequence.
ACCESSION      CF512147
VERSION      CF512147.1      GI:34543915
KEYWORDS      EST:
SOURCE      Vitis vinifera
ORGANISM      Vitis vinifera
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE      rosids; Vitaceae; Vitis.
JOURNAL      1 (bases 1 to 722)
COMMENT      Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Jones, K. and
              Cook, D.
              Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
              berries at various developmental stages
              Unpublished (2003)
              Contact: Douglas Cook, PhD
              CAES Genome Facility
              UC Davis, Plant Pathology
              One Shields Ave, Davis, CA 95616, USA
              Tel: 530 754 6561
              Fax: 530 754 6617
              Email: drcook@ucdavis.edu
              Seq primer: GCCAAACGAATGCTCTAG.

```

```

Unpublished (2003)
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
FEATURES      Location/Qualifiers
source      1..722
              /organism="Vitis vinifera"
              /mol_type="mRNA"
              /cultivar="Cabernet Sauvignon (Clone 8)"
              /db_xref="taxon:29760"
              /clone="Cabud0003_IF_A10"
              /sex="Hermaphrodite"
              /dev_stage="Pre-bloom (10-11 days before bloom)"
              /lab_host="DH5alpha"
              /clone_lib="Vitis vinifera cv. cabernet sauvignon (Clone
              8) Bud - CABUD"
              /note="Organ: Bud; Vector: pDNR; Site 1: SfiI; Site 2:
              SfiI; CABUD is a cDNA library of Vitis vinifera cv.
              'Cabernet Sauvignon' Clone 8 dissected buds. Samples were
              collected May 13, 2002 from pre-bloom plants (10-11 days
              before bloom), pre-veraison. Sampled vines were located at
              the University of California, Davis, Experimental
              Vineyard. cDNAs were made by oligo-dT priming and
              directionally cloned. 5' and 3' adaptors were used in
              cloning as follows:
              5'-AAGCAGTGTATCAACGAGAGAGTGGCCATTACGGCGGG-3' and
              5'-ATTCTAGAGCGGCGGCGGACATG-DT(30)NN-3'. Library was
              constructed using the Clontech Creator SMART kit and
              size-selected to contain the 0.5-3 kb size fraction."
ORIGIN
Query Match      70.0%; Score 19.6; DB 14; Length 722;
Best Local Similarity      84.6%; Pred. No. 4.5e+02;
Matches      22; Conservative      0; Mismatches      4; Indels      0; Gaps      0;

QY      1      AATATGCTGAACGCGAGAGAAACCG 26
Db      350      ACTATGCTGAACCTCGAAGAAACTG 325

RESULT 6
CF512236      734 bp      mRNA      linear      EST 09-SEP-2003
LOCUS      Cabud0003_IR_A10 Vitis vinifera cv. cabernet sauvignon (Clone 8)
DEFINITION      Bud - CABUD Vitis vinifera cDNA clone Cabud0003_IR_A10 3', mRNA
              sequence.
ACCESSION      CF512236
VERSION      CF512236.1      GI:34544004
KEYWORDS      EST:
SOURCE      Vitis vinifera
ORGANISM      Vitis vinifera
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE      rosids; Vitaceae; Vitis.
JOURNAL      1 (bases 1 to 734)
COMMENT      Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Jones, K. and
              Cook, D.
              Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
              berries at various developmental stages
              Unpublished (2003)
              Contact: Douglas Cook, PhD
              CAES Genome Facility
              UC Davis, Plant Pathology
              One Shields Ave, Davis, CA 95616, USA
              Tel: 530 754 6561
              Fax: 530 754 6617
              Email: drcook@ucdavis.edu
              Seq primer: GCCAAACGAATGCTCTAG.

```


VERSION	AL466434.1	GI:11835789
KEYWORDS	GSS.	
SOURCE	Trypanosoma brucei	
ORGANISM	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.	
REFERENCE	1 (bases 1 to 576)	
AUTHORS	Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.	
TITLE	Direct Submission	
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk	
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.	
FEATURES	source	
	1..576	
	/organism="Trypanosoma brucei"	
	/mol_type="genomic DNA"	
	/strain="TREU927"	
	/db_xref="taxon:5691"	
	/clone="140d12"	
ORIGIN		
	Query Match 67.9%; Score 19; DB 29; Length 576;	
	Best Local Similarity 81.5%; Pred. No. 7.9e+02;	
	Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
QY	2 ATATGCTGAAACGCGAGAGAAACCGCG 28	
DBD	231 ATATCAGAAACGCGAGAGCAAGGACG 257	
RESULT 11		
BE776235		
LOCUS	BE776235	580 bp mRNA linear EST 20-SEP-2000
DEFINITION	MY-12-F-04 PinfeetansMY Phytophthora infestans cDNA, mRNA sequence.	
ACCESSION	BE776235	
VERSION	BE776235.1	GI:10229890
KEYWORDS	EST.	
SOURCE	Phytophthora infestans (potato late blight agent)	
ORGANISM	Phytophthora infestans	
	Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Phytophthora.	
REFERENCE	1 (bases 1 to 580)	
AUTHORS	Kamoun, S., Hrabet, P.T., Sobral, B.W.S., Nuss, D. and Govers, F.	
TITLE	Initial assessment of gene diversity for the oomycete pathogen Phytophthora infestans based on expressed sequences	
JOURNAL	Fungal Genet. Biol. 28 (2): 94-106 (1999)	
MEDLINE	20056376	
PUBMED	10587472	
COMMENT	Contact: Govers F Laboratory of Phytopathology Wageningen University Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands Tel: 31 317 483 138 Fax: 31 317 483 412 Email: Francine.Govers@medew.fyto.wau.nl.	
FEATURES	source	
	1..580	
	/organism="Phytophthora infestans"	

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